

SEQUENCE LISTING

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Steele, Christopher L  
Phillips, Michael A

<120> MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)

<130> WSUR18414

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<150> 09/360,545

<151> 1999-07-26

<150> 60/052,249

<151> 1997-07-11

<150> PCT/US98/14528

<151> 1998-07-10

<160> 107

<170> PatentIn Ver. 2.0

<210> 1

<211> 2196

<212> DNA

<213> Abies grandis

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<222> (69)..(1952)

<223> Clone AG2.2 encoding myrcene synthase

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Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys  
1 5 10

ctg cgc aag tcg ttg atc agt tca att cat gaa cat aag cct ccc tat 158  
Leu Arg Lys Ser Leu Ile Ser Ser Ile His Gln His Lys Pro Pro Tyr  
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aga aca atc cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg 206  
Arg Thr Ile Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr  
35 40 45

cct tcc atg agc atc agt ttg gcc acc gct gca cct gat gat ggt gta 254  
Pro Ser Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val  
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caa aga cgc ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc 302  
Gln Arg Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe  
65 70 75

ata cag tct cta tca acg cct tat ggg gaa ccc tct tac cag gaa cgt 350

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Ala	Glu	Arg	Leu	Ile	Val	Glu	Val	Lys	Lys	Ile	Phe	Asn	Ser	Met	Tyr	
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ctg	gat	gat	gga	aga	tta	atg	agt	tcc	ttt	aat	gat	ctc	atg	caa	cgc	446
Leu	Asp	Asp	Gly	Arg	Leu	Met	Ser	Ser	Phe	Asn	Asp	Leu	Met	Gln	Arg	
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ctt	tgg	ata	gtc	gat	agc	gtt	gaa	cgt	ttg	ggg	ata	gct	aga	cat	ttc	494
Leu	Trp	Ile	Val	Asp	Ser	Val	Glu	Arg	Leu	Gly	Ile	Ala	Arg	His	Phe	
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Lys	Asn	Glu	Ile	Thr	Ser	Ala	Leu	Asp	Tyr	Val	Phe	Arg	Tyr	Trp	Glu	
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Glu	Asn	Gly	Ile	Gly	Cys	Gly	Arg	Asp	Ser	Ile	Val	Thr	Asp	Leu	Asn	
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Ser	Thr	Ala	Leu	Gly	Phe	Arg	Thr	Leu	Arg	Leu	His	Gly	Tyr	Thr	Val	
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Ser	Pro	Glu	Val	Leu	Lys	Ala	Phe	Gln	Asp	Gln	Asn	Gly	Gln	Phe	Val	
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Cys	Ser	Pro	Gly	Gln	Thr	Glu	Gly	Glu	Ile	Arg	Ser	Val	Leu	Asn	Leu	
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Tyr	Arg	Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu	Glu	
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gct	gaa	atc	ttc	tcc	aca	aga	tat	ttg	aaa	gaa	gct	cta	caa	aag	att	830
Ala	Glu	Ile	Phe	Ser	Thr	Arg	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Lys	Ile	
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Pro	Val	Ser	Ala	Leu	Ser	Gln	Glu	Ile	Lys	Phe	Val	Met	Glu	Tyr	Gly	
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tgg	cac	aca	aat	ttg	cca	aga	ttg	gaa	gca	aga	aat	tac	ata	gac	aca	926
Trp	His	Thr	Asn	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Asp	Thr	
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Leu	Glu	Lys	Asp	Thr	Ser	Ala	Trp	Leu	Asn	Lys	Asn	Ala	Gly			

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Pro Lys Leu Thr Phe	Ala Arg His Arg His	Val Glu Phe Tyr Thr Leu	
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gcc tct tgt att gcc att gac	cca aaa cat tct gca ttc	aga cta ggc	1166
Ala Ser Cys Ile Ala Ile Asp	Pro Lys His Ser Ala Phe	Arg Leu Gly	
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ttc gcc aaa atg tgt cat ctt gtc	aca gtt ttg gac gat att tac gac		1214
Phe Ala Lys Met Cys His Leu Val	Thr Val Leu Asp Asp Ile Tyr Asp		
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Thr Phe Gly Thr Ile Asp Glu	Leu Glu Leu Phe Thr Ser Ala Ile Lys		
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Arg Trp Asn Ser Ser Glu Ile Glu	His Leu Pro Glu Tyr Met Lys Cys		
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gtg tac atg gtc gtg ttt gaa act	gta aat gaa ctg aca cga gag gcg		1358
Val Tyr Met Val Val Phe Glu Thr	Val Asn Glu Leu Thr Arg Glu Ala		
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Glu Lys Thr Gln Gly Arg Asn Thr	Leu Asn Tyr Val Arg Lys Ala Trp		
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gag gct tat ttt gat tca tat atg	gaa gaa gca aaa tgg atc tct aat		1454
Glu Ala Tyr Phe Asp Ser Tyr Met	Glu Glu Ala Lys Trp Ile Ser Asn		
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Gly Tyr Leu Pro Met Phe Glu Glu	Tyr His Glu Asn Gly Lys Val Ser		
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Ser Ala Tyr Arg Val Ala Thr Leu	Gln Pro Ile Leu Thr Leu Asn Ala		
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Trp Leu Pro Asp Tyr Ile Leu Lys	Gly Ile Asp Phe Pro Ser Arg Phe		
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Asn Asp Leu Ala Ser Ser Phe Leu	Arg Leu Arg Gly Asp Thr Arg Cys		
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Tyr Lys Ala Asp Arg Asp Arg Gly	Glu Glu Ala Ser Cys Ile Ser Cys		
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tat atg aaa gac aat cct gga tca	acc gaa gaa gat gcc ctc aat cat		1742
Tyr Met Lys Asp Asn Pro Gly Ser	Thr Glu Glu Asp Ala Leu Asn His		
545	550	555	
atc aat gcc atg gtc aat gac ata	atc aaa gaa tta aat tgg gaa ctt		1790
Ile Asn Ala Met Val Asn Asp Ile	Ile Lys Glu Leu Asn Trp Glu Leu		
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 Asp Ile Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe  
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 Glu Ser Met Leu Phe  
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Ile Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr Pro Ser  
 35 40 45

Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg  
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Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln  
 65 70 75 80

Ser Leu Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu  
 85 90 95

Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp  
 100 105 110

Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp  
 115 120 125

Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn  
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Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn  
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Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr  
165 170 175

Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val Ser Pro  
180 185 190

Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val Cys Ser  
195 200 205

Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu Tyr Arg  
210 215 220

Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu  
225 230 235 240

Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro Val  
245 250 255

Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly Trp His  
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Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys Leu Leu  
290 295 300

Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln Gln Lys  
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Glu Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu Pro Lys  
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Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu Ala Ser  
340 345 350

Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala  
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Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe  
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Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp  
385 390 395 400

Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr  
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Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala Glu Lys  
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Leu Pro Met Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala  
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gag Glu	aaa Lys	ctg Leu	atc Ile	ggg Gly 100	gaa Glu	gta Val	aag Lys	aac Asn 105	atg Met	ttc Phe	aat Asn	tcg Ser	atg Met	tca Ser 110	tta Leu	338
gaa Glu	gat Asp	gga Gly	gag Glu 115	tta Leu	atg Met	agt Ser	ccg Pro	ctc Leu 120	aat Asn	gat Asp	ctc Leu	att Ile	caa Gln 125	cgc Arg	ctt Leu	386
tgg Trp	att Ile	gtc Val 130	gac Asp	agc Ser	ctt Leu	gaa Glu 135	cgt Arg	ttg Leu	ggg Gly	atc Ile	cat His 140	aga Arg	cat His	ttc Phe	aaa Lys	434
gat Asp	gag Glu 145	ata Ile	aaa Lys	tcg Ser	gcg Ala	ctt Leu 150	gat Asp	tat Tyr	gtt Val	tac Tyr	agt Ser 155	tat Tyr	tgg Trp	ggc Gly	gaa Glu	482
aat Asn 160	ggc Gly	atc Ile	gga Gly	tgc Cys	ggg Gly 165	agg Arg	gag Glu	agt Ser	gtt Val 170	gtt Val	act Thr	gat Asp	ctg Leu	aac Asn 175	tca Ser	530
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tca Ser	gat Asp	gtt Val 195	ttc Phe	aaa Lys	gct Ala	ttc Phe	aaa Lys 200	ggc Gly	caa Gln	aat Asn	ggg Gly	cag Gln	ttt Phe 205	tcc Ser	tgc Cys	626
tct Ser	gaa Glu 210	aat Asn	att Ile	cag Gln	aca Thr	gat Asp 215	gaa Glu	gag Glu	atc Ile	aga Arg	ggc Gly 220	gtt Val	ctg Leu	aat Asn	tta Leu	674
ttc Phe 225	cgg Arg	gcc Ala	tcc Ser	ctc Leu	att Ile	gcc Ala 230	ttt Phe	cca Pro	ggg Gly	gag Glu	aaa Lys 235	att Ile	atg Met	gat Asp	gag Glu	722
gct Ala 240	gaa Glu	atc Ile	ttc Phe	tct Ser	acc Thr 245	aaa Lys	tat Tyr	tta Leu	aaa Lys 250	gaa Glu	gcc Ala	ctg Leu	caa Gln	aag Lys	att Ile 255	770
ccg Pro	gtc Val	tcc Ser	agt Ser	ctt Leu 260	tcg Ser	cga Arg	gag Glu	atc Ile	ggg Gly 265	gac Asp	gtt Val	ttg Leu	gaa Glu	tat Tyr 270	ggt Gly	818
tgg Trp	cac His	aca Thr	tat Tyr 275	ttg Leu	ccg Pro	cga Arg	ttg Leu 280	gaa Glu	gca Ala	agg Arg	aat Asn	tac Tyr	atc Ile 285	caa Gln	gtc Val	866
ttt Phe	gga Gly	cag Gln 290	gac Asp	act Thr	gag Glu	aac Asn 295	acg Thr	aag Lys	tca Ser	tat Tyr	gtg Val 300	aag Lys	agc Ser	aaa Lys	aaa Lys	914
ctt Leu	tta Leu 305	gaa Glu	ctc Leu	gca Ala	aaa Lys 310	ttg Leu	gag Glu	ttc Phe	aac Asn	atc Ile 315	ttt Phe	caa Gln	tcc Ser	tta Leu	caa Gln	962

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Lys Arg Glu Leu Glu Ser Leu Val Arg Trp Trp Lys Glu Ser Gly Phe	
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Pro Glu Met Thr Phe Cys Arg His Arg His Val Glu Tyr Tyr Thr Leu	
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Thr Phe Gly Thr Val Asp Glu Leu Glu Leu Phe Thr Ala Thr Met Lys	
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Val	Ser	Ser	Leu	Ser	Arg	Glu	Ile	Gly	Asp	Val	Leu	Glu	Tyr	Gly	Trp				
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His	Thr	Tyr	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Gln	Val	Phe				
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<210> 5  
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<213> Abies grandis

<220>  
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<222> (73)..(1986)  
<223> Clone AG10 encoding limonene synthase

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Met Ala Leu Leu Ser Ile Val Ser Leu Gln Val Pro Lys  
1 5 10

tcc tgc ggg ctg aaa tcg ttg atc agt tcc agc aat gtg cag aag gct 159  
Ser Cys Gly Leu Lys Ser Leu Ile Ser Ser Ser Asn Val Gln Lys Ala  
15 20 25

ctc tgt atc tct aca gca gtc cca aca ctc aga atg cgt agg cga cag 207  
Leu Cys Ile Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln  
30 35 40 45

aaa gct ctg gtc atc aac atg aaa ttg acc act gta tcc cat cgt gat 255  
Lys Ala Leu Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp  
50 55 60

gat aat ggt ggt ggt gta ctg caa aga cgc ata gcc gat cat cat ccc 303  
Asp Asn Gly Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro  
65 70 75

aac ctg tgg gaa gat gat ttc ata caa tca ttg tcc tca cct tat ggg	351
Asn Leu Trp Glu Asp Asp Phe Ile Gln Ser Leu Ser Ser Pro Tyr Gly	
80 85 90	
gga tct tcg tac agt gaa cgt gct gag aca gtc gtt gag gaa gta aaa	399
Gly Ser Ser Tyr Ser Glu Arg Ala Glu Thr Val Val Glu Glu Val Lys	
95 100 105	
gag atg ttc aat tca ata cca aat aat aga gaa tta ttt ggt tcc caa	447
Glu Met Phe Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln	
110 115 120 125	
aat gat ctc ctt aca cgc ctt tgg atg gtg gat agc att gaa cgt ctg	495
Asn Asp Leu Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu	
130 135 140	
ggg ata gat aga cat ttc caa aat gag ata aga gta gcc ctc gat tat	543
Gly Ile Asp Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr	
145 150 155	
gtt tac agt tat tgg aag gaa aag gaa ggc att ggg tgt ggc aga gat	591
Val Tyr Ser Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp	
160 165 170	
tct act ttt cct gat ctc aac tcg act gcc ttg gcg ctt cga act ctt	639
Ser Thr Phe Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu	
175 180 185	
cga ctg cac gga tac aat gtg tct tca gat gtg ctg gaa tac ttc aaa	687
Arg Leu His Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys	
190 195 200 205	
gat gaa aag ggg cat ttt gcc tgc cct gca atc cta acc gag gga cag	735
Asp Glu Lys Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln	
210 215 220	
atc act aga agt gtt cta aat tta tat cgg gct tcc ctg gtc gcc ttt	783
Ile Thr Arg Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe	
225 230 235	
ccc ggg gag aaa gtt atg gaa gag gct gaa atc ttc tcg gca tct tat	831
Pro Gly Glu Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ala Ser Tyr	
240 245 250	
ttg aaa aaa gtc tta caa aag att ccg gtc tcc aat ctt tca gga gag	879
Leu Lys Lys Val Leu Gln Lys Ile Pro Val Ser Asn Leu Ser Gly Glu	
255 260 265	
ata gaa tat gtt ttg gaa tat ggt tgg cac acg aat ttg ccg aga ttg	927
Ile Glu Tyr Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu	
270 275 280 285	
gaa gca aga aat tat atc gag gtc tac gag cag agc ggc tat gaa agc	975
Glu Ala Arg Asn Tyr Ile Glu Val Tyr Glu Gln Ser Gly Tyr Glu Ser	
290 295 300	
tta aac gag atg cca tat atg aac atg aag aag ctt tta caa ctt gca	1023
Leu Asn Glu Met Pro Tyr Met Asn Met Lys Lys Leu Leu Gln Leu Ala	
305 310 315	

aaa ttg gag ttc aat atc ttt cac tct ttg caa cta aga gag tta caa	1071
Lys Leu Glu Phe Asn Ile Phe His Ser Leu Gln Leu Arg Glu Leu Gln	
320 325 330	
tct atc tcc aga tgg tgg aaa gaa tca ggt tcc tct caa ctg act ttt	1119
Ser Ile Ser Arg Trp Trp Lys Glu Ser Gly Ser Ser Gln Leu Thr Phe	
335 340 345	
aca cgg cat cgt cac gtg gaa tac tac act atg gca tct tgc att tct	1167
Thr Arg His Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser	
350 355 360 365	
atg ttg cca aaa cat tca gct ttc aga atg gag ttt gtc aaa gtg tgt	1215
Met Leu Pro Lys His Ser Ala Phe Arg Met Glu Phe Val Lys Val Cys	
370 375 380	
cat ctt gta aca gtt ctc gat gat ata tat gac act ttt gga aca atg	1263
His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly Thr Met	
385 390 395	
aac gaa ctc caa ctt ttt acg gat gca att aag aga tgg gat ttg tca	1311
Asn Glu Leu Gln Leu Phe Thr Asp Ala Ile Lys Arg Trp Asp Leu Ser	
400 405 410	
acg aca agg tgg ctt cca gaa tat atg aaa gga gtg tac atg gac ttg	1359
Thr Thr Arg Trp Leu Pro Glu Tyr Met Lys Gly Val Tyr Met Asp Leu	
415 420 425	
tat caa tgc att aat gaa atg gtg gaa gag gct gag aag act caa ggc	1407
Tyr Gln Cys Ile Asn Glu Met Val Glu Glu Ala Glu Lys Thr Gln Gly	
430 435 440 445	
cga gat atg ctc aac tat att caa aat gct tgg gaa gcc cta ttt gat	1455
Arg Asp Met Leu Asn Tyr Ile Gln Asn Ala Trp Glu Ala Leu Phe Asp	
450 455 460	
acc ttt atg caa gaa gca aag tgg atc tcc agc agt tat ctc cca acg	1503
Thr Phe Met Gln Glu Ala Lys Trp Ile Ser Ser Ser Tyr Leu Pro Thr	
465 470 475	
ttt gag gag tac ttg aag aat gca aaa gtt agt tct ggt tct cgc ata	1551
Phe Glu Glu Tyr Leu Lys Asn Ala Lys Val Ser Ser Gly Ser Arg Ile	
480 485 490	
gcc aca tta caa ccc att ctc act ttg gat gta cca ctt cct gat tac	1599
Ala Thr Leu Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asp Tyr	
495 500 505	
ata ctg caa gaa att gat tat cca tcc aga ttc aat gag tta gct tcc	1647
Ile Leu Gln Glu Ile Asp Tyr Pro Ser Arg Phe Asn Glu Leu Ala Ser	
510 515 520 525	
tcc atc ctt cga cta cga ggt gac acg cgc tgc tac aag gcg gat agg	1695
Ser Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg	
530 535 540	
gcc cgt gga gaa gaa gct tca gct ata tcc tgt tat atg aaa gac cat	1743
Ala Arg Gly Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His	
545 550 555	
cct gga tca ata gag gaa gat gct ctc aat cat atc aac gcc atg atc	1791

1071 1119 1167 1215 1263 1311 1359 1407 1455 1503 1551 1599 1647 1695 1743 1791

Pro Gly Ser Ile Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile  
560 565 570

agt gat gca atc aga gaa tta aat tgg gag ctt ctc aga ccg gat agc 1839  
Ser Asp Ala Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser  
575 580 585

aaa agt ccc atc tct tcc aag aaa cat gct ttt gac atc acc aga gct 1887  
Lys Ser Pro Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala  
590 595 600 605

ttc cat cat gtc tac aaa tat cga gat ggt tac act gtt tcc aac aac 1935  
Phe His His Val Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ser Asn Asn  
610 615 620

gaa aca aag aat ttg gtg atg aaa acc gtt ctt gaa cct ctc gct ttg 1983  
Glu Thr Lys Asn Leu Val Met Lys Thr Val Leu Glu Pro Leu Ala Leu  
625 630 635

tta aaacatatag aatgcattaa aatgtgggaa gtctataatc tagactattc 2036

tctatctttc ataatgtaga tctggatgtg tattgaactc taaaaaaaaa aaa 2089

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<213> Abies grandis

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Leu Lys Ser Leu Ile Ser Ser Ser Asn Val Gln Lys Ala Leu Cys Ile  
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Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln Lys Ala Leu  
35 40 45

Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp Asp Asn Gly  
50 55 60

Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro Asn Leu Trp  
65 70 75 80

Glu Asp Asp Phe Ile Gln Ser Leu Ser Ser Pro Tyr Gly Gly Ser Ser  
85 90 95

Tyr Ser Glu Arg Ala Glu Thr Val Val Glu Glu Val Lys Glu Met Phe  
100 105 110

Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln Asn Asp Leu  
115 120 125

Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu Gly Ile Asp  
130 135 140

Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr Val Tyr Ser  
145 150 155 160

1000  
900  
800  
700  
600  
500  
400  
300  
200  
100  
0

Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp Ser Thr Phe  
 165 170 175  
 Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu Arg Leu His  
 180 185 190  
 Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys Asp Glu Lys  
 195 200 205  
 Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln Ile Thr Arg  
 210 215 220  
 Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe Pro Gly Glu  
 225 230 235 240  
 Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ala Ser Tyr Leu Lys Lys  
 245 250 255  
 Val Leu Gln Lys Ile Pro Val Ser Asn Leu Ser Gly Glu Ile Glu Tyr  
 260 265 270  
 Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg  
 275 280 285  
 Asn Tyr Ile Glu Val Tyr Glu Gln Ser Gly Tyr Glu Ser Leu Asn Glu  
 290 295 300  
 Met Pro Tyr Met Asn Met Lys Lys Leu Leu Gln Leu Ala Lys Leu Glu  
 305 310 315 320  
 Phe Asn Ile Phe His Ser Leu Gln Leu Arg Glu Leu Gln Ser Ile Ser  
 325 330 335  
 Arg Trp Trp Lys Glu Ser Gly Ser Ser Gln Leu Thr Phe Thr Arg His  
 340 345 350  
 Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser Met Leu Pro  
 355 360 365  
 Lys His Ser Ala Phe Arg Met Glu Phe Val Lys Val Cys His Leu Val  
 370 375 380  
 Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly Thr Met Asn Glu Leu  
 385 390 395 400  
 Gln Leu Phe Thr Asp Ala Ile Lys Arg Trp Asp Leu Ser Thr Thr Arg  
 405 410 415  
 Trp Leu Pro Glu Tyr Met Lys Gly Val Tyr Met Asp Leu Tyr Gln Cys  
 420 425 430  
 Ile Asn Glu Met Val Glu Glu Ala Glu Lys Thr Gln Gly Arg Asp Met  
 435 440 445  
 Leu Asn Tyr Ile Gln Asn Ala Trp Glu Ala Leu Phe Asp Thr Phe Met  
 450 455 460  
 Gln Glu Ala Lys Trp Ile Ser Ser Ser Tyr Leu Pro Thr Phe Glu Glu  
 465 470 475 480  
 Tyr Leu Lys Asn Ala Lys Val Ser Ser Gly Ser Arg Ile Ala Thr Leu

485

490

495

Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asp Tyr Ile Leu Gln  
500 505 510

Glu Ile Asp Tyr Pro Ser Arg Phe Asn Glu Leu Ala Ser Ser Ile Leu  
515 520 525

Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Ala Arg Gly  
530 535 540

Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His Pro Gly Ser  
545 550 555 560

Ile Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile Ser Asp Ala  
565 570 575

Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser Lys Ser Pro  
580 585 590

Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala Phe His His  
595 600 605

Val Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ser Asn Asn Glu Thr Lys  
610 615 620

Asn Leu Val Met Lys Thr Val Leu Glu Pro Leu Ala Leu  
625 630 635

<210> 7

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Degenerate  
oligonucleotide PCR primer A wherein the letter  
"n" indicates an inosine residue

<220>

<221> misc\_feature

<222> (1)..(25)

<223> Degenerate oligonucleotide Primer A wherein n  
represents inosine

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arraygarra nggnrartay aarga

25

<210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: degenerate  
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"n" represents an inosine residue

<220>



<221> misc\_feature  
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represents an inosine residue

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<210> 9  
<211> 24  
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"n" represents an inosine residue

<220>  
<221> misc\_feature  
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<400> 9  
ctnkynrang gncratrta ckty 24

<210> 10  
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<223> Description of Artificial Sequence: degenerate  
oligonucleotide PCR primer D wherein the letter  
"n" represents an inosine residue

<220>  
<221> misc\_feature  
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inosine

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<211> 108  
<212> DNA  
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<210> 12



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Asn	Pro	Ala	Ile	Thr	Gly	Asp	Gly	Glu	Ser	Met	Ile	Thr	Pro	Ser	Ala	
		35					40					45				
tat	gac	aca	gca	tgg	gta	gcg	agg	gtg	ccc	gcc	att	gat	ggc	tct	gct	193
Tyr	Asp	Thr	Ala	Trp	Val	Ala	Arg	Val	Pro	Ala	Ile	Asp	Gly	Ser	Ala	
	50					55					60					
cgc	ccg	caa	ttt	ccc	caa	aca	gtt	gac	tgg	att	ttg	aaa	aac	cag	tta	241
Arg	Pro	Gln	Phe	Pro	Gln	Thr	Val	Asp	Trp	Ile	Leu	Lys	Asn	Gln	Leu	
65					70					75					80	
aaa	gat	ggt	tca	tgg	gga	att	cag	tcc	cac	ttt	ctg	ctg	tcc	gac	cgt	289
Lys	Asp	Gly	Ser	Trp	Gly	Ile	Gln	Ser	His	Phe	Leu	Leu	Ser	Asp	Arg	
				85					90					95		
ctt	ctt	gcc	act	ctt	tct	tgt	gtt	ctt	gtg	ctc	ctt	aaa	tgg	aac	gtt	337
Leu	Leu	Ala	Thr	Leu	Ser	Cys	Val	Leu	Val	Leu	Leu	Lys	Trp	Asn	Val	
		100					105					110				
ggg	gat	ctg	caa	gta	gag	cag	gga	att	gaa	ttc	ata	aag	agc	aat	ctg	385
Gly	Asp	Leu	Gln	Val	Glu	Gln	Gly	Ile	Glu	Phe	Ile	Lys	Ser	Asn	Leu	
	115					120					125					
gaa	cta	gta	aag	gat	gaa	acc	gat	caa	gat	agc	ttg	gta	aca	gac	ttt	433
Glu	Leu	Val	Lys	Asp	Glu	Thr	Asp	Gln	Asp	Ser	Leu	Val	Thr	Asp	Phe	
130						135					140					
gag	atc	ata	ttt	cct	tct	ctg	tta	aga	gaa	gct	caa	tct	ctg	cgc	ctc	481
Glu	Ile	Ile	Phe	Pro	Ser	Leu	Leu	Arg	Glu	Ala	Gln	Ser	Leu	Arg	Leu	
145					150					155					160	
gga	ctt	ccc	tac	gac	ctg	cct	tat	ata	cat	ctg	ttg	cag	act	aaa	cgg	529
Gly	Leu	Pro	Tyr	Asp	Leu	Pro	Tyr	Ile	His	Leu	Leu	Gln	Thr	Lys	Arg	
			165						170					175		
cag	gaa	aga	tta	gca	aaa	ctt	tca	agg	gag	gaa	att	tat	gcg	gtt	ccg	577
Gln	Glu	Arg	Leu	Ala	Lys	Leu	Ser	Arg	Glu	Glu	Ile	Tyr	Ala	Val	Pro	
		180					185						190			
tcg	cca	ttg	ttg	tat	tct	tta	gag	gga	ata	caa	gat	ata	gtt	gaa	tgg	625
Ser	Pro	Leu	Leu	Tyr	Ser	Leu	Glu	Gly	Ile	Gln	Asp	Ile	Val	Glu	Trp	
	195					200					205					
gaa	cga	ata	atg	gaa	gtt	caa	agt	cag	gat	ggg	tct	ttc	tta	agc	tca	673
Glu	Arg	Ile	Met	Glu	Val	Gln	Ser	Gln	Asp	Gly	Ser	Phe	Leu	Ser	Ser	
210					215					220						
cct	gct	tct	act	gcc	tgc	gtt	ttc	atg	cac	aca	gga	gac	gcg	aaa	tgc	721
Pro	Ala	Ser	Thr	Ala	Cys	Val	Phe	Met	His	Thr	Gly	Asp	Ala	Lys	Cys	
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Ile Val Arg Leu Gly Ile Tyr Arg His Phe Glu Lys Glu Ile Lys Glu	
275	280 285
gct ctt gat tat gtt tac agg cat tgg aac gaa aga gga att ggg tgg	913
Ala Leu Asp Tyr Val Tyr Arg His Trp Asn Glu Arg Gly Ile Gly Trp	
290	295 300
ggc aga cta aat ccc ata gca gat ctt gag acc act gct ttg gga ttt	961
Gly Arg Leu Asn Pro Ile Ala Asp Leu Glu Thr Thr Ala Leu Gly Phe	
305	310 315 320
cga ttg ctt cgg ctg cat agg tac aat gta tct cca gcc att ttt gac	1009
Arg Leu Leu Arg Leu His Arg Tyr Asn Val Ser Pro Ala Ile Phe Asp	
	325 330 335
aac ttc aaa gat gcc aat ggg aaa ttc att tgc tgc acc ggt caa ttc	1057
Asn Phe Lys Asp Ala Asn Gly Lys Phe Ile Cys Ser Thr Gly Gln Phe	
	340 345 350
aac aaa gat gta gca agc atg ctg aat ctt tat aga gct tcc cag ctc	1105
Asn Lys Asp Val Ala Ser Met Leu Asn Leu Tyr Arg Ala Ser Gln Leu	
	355 360 365
gca ttt ccc gga gaa aac att ctt gat gaa gct aaa agc ttc gct act	1153
Ala Phe Pro Gly Glu Asn Ile Leu Asp Glu Ala Lys Ser Phe Ala Thr	
	370 375 380
aaa tat ttg aga gaa gct ctt gag aaa agt gag act tcc agt gca tgg	1201
Lys Tyr Leu Arg Glu Ala Leu Glu Lys Ser Glu Thr Ser Ser Ala Trp	
	385 390 395 400
aac aac aaa caa aac ctg agc caa gag atc aaa tac gcg ctg aag act	1249
Asn Asn Lys Gln Asn Leu Ser Gln Glu Ile Lys Tyr Ala Leu Lys Thr	
	405 410 415
tct tgg cat gcc agt gtt ccg aga gtg gaa gca aag aga tac tgt caa	1297
Ser Trp His Ala Ser Val Pro Arg Val Glu Ala Lys Arg Tyr Cys Gln	
	420 425 430
gtg tat cgc cca gat tat gca cgc ata gca aaa tgc gtt tac aag cta	1345
Val Tyr Arg Pro Asp Tyr Ala Arg Ile Ala Lys Cys Val Tyr Lys Leu	
	435 440 445
ccc tac gtg aac aat gaa aag ttt tta gag ctg gga aaa tta gat ttc	1393
Pro Tyr Val Asn Asn Glu Lys Phe Leu Glu Leu Gly Lys Leu Asp Phe	
	450 455 460
aac att atc cag tcc atc cac caa gaa gaa atg aag aat gtt acc agc	1441
Asn Ile Ile Gln Ser Ile His Gln Glu Glu Met Lys Asn Val Thr Ser	
	465 470 475 480
tgg ttt aga gat tgc ggg ttg cca cta ttc acc ttc gct cgg gag agg	1489
Trp Phe Arg Asp Ser Gly Leu Pro Leu Phe Thr Phe Ala Arg Glu Arg	
	485 490 495
ccg ctg gaa ttc tac ttc tta gta gcg gcg ggg acc tat gaa ccc cag	1537
Pro Leu Glu Phe Tyr Phe Leu Val Ala Ala Gly Thr Tyr Glu Pro Gln	
	500 505 510
tat gcc aaa tgc agg ttc ctc ttt aca aaa gtg gca tgc ttg cag act	1585
Tyr Ala Lys Cys Arg Phe Leu Phe Thr Lys Val Ala Cys Leu Gln Thr	

Case	Age	Sex	Occupation	Duration of illness	Site of lesion	Pathological findings	Microscopic findings	Immunohistochemical findings	Diagnosis
1	45	M	Farmer	10 years	Right lower leg	Chronic inflammation	Neutrophils, monocytes	CD45, CD68	Chronic inflammation
2	52	F	Housewife	5 years	Left lower leg	Chronic inflammation	Neutrophils, monocytes	CD45, CD68	Chronic inflammation
3	68	M	Retired	15 years	Right lower leg	Chronic inflammation	Neutrophils, monocytes	CD45, CD68	Chronic inflammation
4	72	F	Housewife	20 years	Left lower leg	Chronic inflammation	Neutrophils, monocytes	CD45, CD68	Chronic inflammation
5	78	M	Farmer	25 years	Right lower leg	Chronic inflammation	Neutrophils, monocytes	CD45, CD68	Chronic inflammation
6	82	F	Housewife	30 years	Left lower leg	Chronic inflammation	Neutrophils, monocytes	CD45, CD68	Chronic inflammation
7	85	M	Retired	35 years	Right lower leg	Chronic inflammation	Neutrophils, monocytes	CD45, CD68	Chronic inflammation
8	88	F	Housewife	40 years	Left lower leg	Chronic inflammation	Neutrophils, monocytes	CD45, CD68	Chronic inflammation
9	90	M	Farmer	45 years	Right lower leg	Chronic inflammation	Neutrophils, monocytes	CD45, CD68	Chronic inflammation
10	92	F	Housewife	50 years	Left lower leg	Chronic inflammation	Neutrophils, monocytes	CD45, CD68	Chronic inflammation

aaa gat cat atc aaa gag tgt ctc att gaa ccg ctg cca ctg taa 2350  
 Lys Asp His Ile Lys Glu Cys Leu Ile Glu Pro Leu Pro Leu  
 770 775 780

tcaaaatagt tgcaataata attgaaataa tgtcaactat gtttcacaaa aaaaaaaaaa 2410

aaaaaaaaaa aaaa 2424

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 <212> PRT  
 <213> Abies grandis

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 35 40 45

Tyr Asp Thr Ala Trp Val Ala Arg Val Pro Ala Ile Asp Gly Ser Ala  
 50 55 60

Arg Pro Gln Phe Pro Gln Thr Val Asp Trp Ile Leu Lys Asn Gln Leu  
 65 70 75 80

Lys Asp Gly Ser Trp Gly Ile Gln Ser His Phe Leu Leu Ser Asp Arg  
 85 90 95

Leu Leu Ala Thr Leu Ser Cys Val Leu Val Leu Leu Lys Trp Asn Val  
 100 105 110

Gly Asp Leu Gln Val Glu Gln Gly Ile Glu Phe Ile Lys Ser Asn Leu  
 115 120 125

Glu Leu Val Lys Asp Glu Thr Asp Gln Asp Ser Leu Val Thr Asp Phe  
 130 135 140

Glu Ile Ile Phe Pro Ser Leu Leu Arg Glu Ala Gln Ser Leu Arg Leu  
 145 150 155 160

Gly Leu Pro Tyr Asp Leu Pro Tyr Ile His Leu Leu Gln Thr Lys Arg  
 165 170 175

Gln Glu Arg Leu Ala Lys Leu Ser Arg Glu Glu Ile Tyr Ala Val Pro  
 180 185 190

Ser Pro Leu Leu Tyr Ser Leu Glu Gly Ile Gln Asp Ile Val Glu Trp  
 195 200 205

Glu Arg Ile Met Glu Val Gln Ser Gln Asp Gly Ser Phe Leu Ser Ser  
 210 215 220

Pro Ala Ser Thr Ala Cys Val Phe Met His Thr Gly Asp Ala Lys Cys  
 225 230 235 240

Leu	Glu	Phe	Leu	Asn	Ser	Val	Met	Ile	Lys	Phe	Gly	Asn	Phe	Val	Pro	
				245					250						255	
Cys	Leu	Tyr	Pro	Val	Asp	Leu	Leu	Glu	Arg	Leu	Leu	Ile	Val	Asp	Asn	
			260					265					270			
Ile	Val	Arg	Leu	Gly	Ile	Tyr	Arg	His	Phe	Glu	Lys	Glu	Ile	Lys	Glu	
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Val Trp Asp Asp Asp Leu Ile His Ser Leu Asn Ser Pro Tyr Gly Ala  
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Pro Ala Tyr Tyr Glu Leu Leu Gln Lys Leu Ile Glu Glu Ile Lys His	
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Leu Leu Leu Thr Glu Met Glu Met Asp Asp Gly Asp His Asp Leu Ile	
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Lys Arg Leu Gln Ile Val Asp Thr Leu Glu Cys Leu Gly Ile Asp Arg	
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Ser	Leu	Leu	Glu	Arg	Gly	Glu	Val	Arg	Ile	Gly	Val	Ser	Met	Ala	Cys	
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[illegible]

Val Arg Ser Met Leu Ser Leu Leu Arg Ala Ser Glu Ile Ser Phe Pro  
165 170 175

Gly Glu Lys Val Met Glu Glu Ala Lys Ala Phe Thr Arg Glu Tyr Leu  
180 185 190

Asn Gln Val Leu Ala Gly His Gly Asp Val Thr Asp Val Asp Gln Ser  
195 200 205

Leu Leu Glu Arg Gly Glu Val Arg Ile Gly Val Ser Met Ala Cys Ser  
210 215 220

Val Pro Arg Trp Glu Ala Arg Ser Phe Leu Glu Ile Tyr Gly His Asn  
225 230 235 240

His Ser Trp Leu Lys Ser Asn Ile Asn Gln Lys Met Leu Lys Leu Ala  
245 250 255

Lys Leu Asp Phe Asn Ile Leu Gln Cys Lys His His Lys Glu Ile Gln  
260 265 270

Phe Ile Thr Arg Trp Trp Arg Asp Ser Gly Ile Ser Gln Leu Asn Phe  
275 280 285

Tyr Arg Lys Arg His Val Glu Tyr Tyr Ser Trp Val Val Met Cys Ile  
290 295 300

Phe Glu Pro Glu Phe Ser Glu Ser Arg Ile Ala Phe Ala Lys Thr Ala  
305 310 315 320

Ile Leu Cys Thr Val Leu Asp Asp Leu Tyr Asp Thr His Ala Thr Leu  
325 330 335

His Glu Ile Lys Ile Met Thr Glu Gly Val Arg Arg Trp Asp Leu Ser  
340 345 350

Leu Thr Asp Asp Leu Pro Asp Tyr Ile Lys Ile Ala Phe Gln Phe Phe  
355 360 365

Phe Asn Thr Val Asn Glu Leu Ile Val Glu Ile Val Lys Arg Gln Gly  
370 375 380

Arg Asp Met Thr Thr Ile Val Lys Asp Cys Trp Lys Arg Tyr Ile Glu  
385 390 395 400

Ser Tyr Leu Gln Glu Ala Glu Trp Ile Ala Thr Gly His Ile Pro Thr  
405 410 415

Phe Asn Glu Tyr Ile Lys Asn Gly Met Ala Ser Ser Gly Met Cys Ile  
420 425 430

Val Asn Leu Asn Pro Leu Leu Leu Leu Gly Lys Leu Leu Pro Asp Asn  
435 440 445

Ile Leu Glu Gln Ile His Ser Pro Ser Lys Ile Leu Asp Leu Leu Glu  
450 455 460

Leu Thr Gly Arg Ile Ala Asp Asp Leu Lys Asp Phe Glu Asp Glu Lys  
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Pro	Glu	Phe	Ser	Gly	Ser	Arg	Val	Ala	Phe	Thr	Lys	Ile	Ala	Ile	Leu		
		130					135					140					
atg	aca	atg	cta	gat	gac	ctg	tac	gat	act	cac	gga	acc	ttg	gac	caa	479	
Met	Thr	Met	Leu	Asp	Asp	Leu	Tyr	Asp	Thr	His	Gly	Thr	Leu	Asp	Gln		
	145					150					155						
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Leu	Lys	Ile	Phe	Thr	Glu	Gly	Val	Arg	Arg	Trp	Asp	Val	Ser	Leu	Val		
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gag	ggc	ctc	cca	gac	ttc	atg	aaa	att	gca	ttc	gag	ttc	tgg	tta	aag	575	
Glu	Gly	Leu	Pro	Asp	Phe	Met	Lys	Ile	Ala	Phe	Glu	Phe	Trp	Leu	Lys		
			180						185					190			
aca	tct	aat	gaa	ttg	att	gct	gaa	gct	gtt	aaa	gcg	caa	ggg	caa	gat	623	
Thr	Ser	Asn	Glu	Leu	Ile	Ala	Glu	Ala	Val	Lys	Ala	Gln	Gly	Gln	Asp		
			195					200					205				
atg	gcg	gcc	tac	ata	aga	aaa	aat	gca	tgg	gag	cga	tac	ctt	gaa	gct	671	
Met	Ala	Ala	Tyr	Ile	Arg	Lys	Asn	Ala	Trp	Glu	Arg	Tyr	Leu	Glu	Ala		
	210						215					220					
tat	ctg	caa	gat	gcg	gaa	tgg	ata	gcc	act	gga	cat	gtc	ccc	acc	ttt	719	
Tyr	Leu	Gln	Asp	Ala	Glu	Trp	Ile	Ala	Thr	Gly	His	Val	Pro	Thr	Phe		
	225					230					235						
gat	gag	tac	ttg	aat	aat	ggc	aca	cca	aac	act	ggg	atg	tgt	gta	ttg	767	
Asp	Glu	Tyr	Leu	Asn	Asn	Gly	Thr	Pro	Asn	Thr	Gly	Met	Cys	Val	Leu		
240				245						250				255			
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Asn	Leu	Ile	Pro	Leu	Leu	Leu	Met	Gly	Glu	His	Leu	Pro	Ile	Asp	Ile		
			260					265						270			
ctg	gag	caa	ata	ttc	ttg	ccc	tcc	agg	ttc	cac	cat	ctc	att	gaa	ttg	863	
Leu	Glu	Gln	Ile	Phe	Leu	Pro	Ser	Arg	Phe	His	His	Leu	Ile	Glu	Leu		
			275					280					285				
gct	tcc	agg	ctc	gtc	gat	gac	gcg	aga	gat	ttc	cag	gcg	gag	aag	gat	911	
Ala	Ser	Arg	Leu	Val	Asp	Asp	Ala	Arg	Asp	Phe	Gln	Ala	Glu	Lys	Asp		
		290				295						300					
cat	ggg	gat	tta	tcg	tgt	att	gag	tgt	tat	tta	aaa	gat	cat	cct	gag	959	
His	Gly	Asp	Leu	Ser	Cys	Ile	Glu	Cys	Tyr	Leu	Lys	Asp	His	Pro	Glu		
	305					310					315						
tct	aca	gta	gaa	gat	gct	tta	aat	cat	gtt	aat	ggc	ctc	ctt	ggc	aat	1007	
Ser	Thr	Val	Glu	Asp	Ala	Leu	Asn	His	Val	Asn	Gly	Leu	Leu	Gly	Asn		
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Cys	Leu	Leu	Glu	Met	Asn	Trp	Lys	Phe	Leu	Lys	Lys	Gln	Asp	Ser	Val		
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Pro	Leu	Ser	Cys	Lys	Lys	Tyr	Ser	Phe	His	Val	Leu	Ala	Arg	Ser	Ile		

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 Gln Phe Met Tyr Asn Gln Gly Asp Gly Phe Ser Ile Ser Asn Lys Val  
 370 375 380  
 atc aag gat caa gtg cag aaa gtt ctt att gtc ccc gtg cct att tga 1199  
 Ile Lys Asp Gln Val Gln Lys Val Leu Ile Val Pro Val Pro Ile  
 385 390 395  
 tagtagatac tagatagtag attagtagct attagtattt atttcatatc aatatttact 1259  
 aatgctgatg atgggttaaag tccattcaga ccaatctttg gtttattgga cttaaataaa 1319  
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 ttgaaataac tagcacaact attttagtgt ggttgat 1416

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 <213> Abies grandis

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 35 40 45  
 Trp Glu Ala Arg Ser Phe Ile Glu Ile Phe Gly Gln Ile Asp Ser Glu  
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 Leu Lys Ser Asn Leu Ser Lys Lys Met Leu Glu Leu Ala Lys Leu Asp  
 65 70 75 80  
 Phe Asn Ile Leu Gln Cys Thr His Gln Lys Glu Leu Gln Ile Ile Ser  
 85 90 95  
 Arg Trp Phe Ala Asp Ser Ser Ile Ala Ser Leu Asn Phe Tyr Arg Lys  
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 Cys Tyr Val Glu Phe Tyr Phe Trp Met Ala Ala Ala Ile Ser Glu Pro  
 115 120 125  
 Glu Phe Ser Gly Ser Arg Val Ala Phe Thr Lys Ile Ala Ile Leu Met  
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 Thr Met Leu Asp Asp Leu Tyr Asp Thr His Gly Thr Leu Asp Gln Leu  
 145 150 155 160  
 Lys Ile Phe Thr Glu Gly Val Arg Arg Trp Asp Val Ser Leu Val Glu  
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 Gly Leu Pro Asp Phe Met Lys Ile Ala Phe Glu Phe Trp Leu Lys Thr  
 180 185 190



Ser Asn Glu Leu Ile Ala Glu Ala Val Lys Ala Gln Gly Gln Asp Met  
 195 200 205

Ala Ala Tyr Ile Arg Lys Asn Ala Trp Glu Arg Tyr Leu Glu Ala Tyr  
 210 215 220

Leu Gln Asp Ala Glu Trp Ile Ala Thr Gly His Val Pro Thr Phe Asp  
 225 230 235 240

Glu Tyr Leu Asn Asn Gly Thr Pro Asn Thr Gly Met Cys Val Leu Asn  
 245 250 255

Leu Ile Pro Leu Leu Leu Met Gly Glu His Leu Pro Ile Asp Ile Leu  
 260 265 270

Glu Gln Ile Phe Leu Pro Ser Arg Phe His His Leu Ile Glu Leu Ala  
 275 280 285

Ser Arg Leu Val Asp Asp Ala Arg Asp Phe Gln Ala Glu Lys Asp His  
 290 295 300

Gly Asp Leu Ser Cys Ile Glu Cys Tyr Leu Lys Asp His Pro Glu Ser  
 305 310 315 320

Thr Val Glu Asp Ala Leu Asn His Val Asn Gly Leu Leu Gly Asn Cys  
 325 330 335

Leu Leu Glu Met Asn Trp Lys Phe Leu Lys Lys Gln Asp Ser Val Pro  
 340 345 350

Leu Ser Cys Lys Lys Tyr Ser Phe His Val Leu Ala Arg Ser Ile Gln  
 355 360 365

Phe Met Tyr Asn Gln Gly Asp Gly Phe Ser Ile Ser Asn Lys Val Ile  
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Lys Asp Gln Val Gln Lys Val Leu Ile Val Pro Val Pro Ile  
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 "n" represents an inosine residue

<220>

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<222> (1)..(23)

<223> PCR primer E wherein the letter n represents  
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23

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oligonucleotide primer F wherein the letter "n"  
represents an inosine residue

<220>  
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inosine

<400> 22  
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24

<210> 23  
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oligonucleotide PCR primer G wherein the letter  
"n" represents an inosine residue

<220>  
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<400> 23  
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cacacatatt tgccgcgatt ggaagcaagg aattacatcc aagtctttgg acaggacact 180  
gagaacacga agtcatatgt gaagagcaaa aaacttttag aactcgcaaa attggagttc 240  
aacatctttc aatccttact cgcatatccg cattgcaacc cattctgaca atggacatcc 300  
cctttcctga tcatatcctc aaggaagttg acttcccatc aaagcttaac gacttggcat 360  
gtgccatcct tcgattacga ggtgatacgc ggtgctacaa ggcggacagg gctcgtggag 420  
aagaagcttc ctctatatca tgttatatga aagacaatcc tggagtatca gaggaagatg 480

ctctcgatca tatcaacgcc atgatcagtg acgaagtcaa aggcttcaat tgg

533

<210> 25

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: conserved amino acid motif on which the sequence of Primer D was based, wherein Xaa at position number 3 represents Thr or Ile, Xaa at

position number 4 represents Ile or Tyr or Phe, Xaa at position number 6 represents Ala or Val and Xaa at position number 8 represents Ala or Gly

<220>

<221> SITE

<222> (1)..(8)

<223> conserved amino acid motif on which sequence of primer D was based

<400> 25

Asp Asp Xaa Xaa Asp Xaa Tyr Xaa  
1 5

<210> 26

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: conserved amino acid motif on which the sequence of Primer E was based wherein Xaa at position 3 represents Lys or Thr, Xaa at position 4 represents Val or Ile, Xaa at position 6 represents Glu or Asp

<220>

<221> SITE

<222> (1)..(8)

<223> conserved amino acid sequence on which the sequence of primer E was based

<400> 26

Gly Glu Xaa Xaa Met Xaa Glu Ala  
1 5

<210> 27

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: conserved amino acid sequence on which the sequence of primer F was based wherein Xaa at position 2 represents Phe or Tyr or Asp

Xaa at position 3 represents Ile or Leu, Xaa at position 4 represents Thr or Leu  
or Arg

<220>  
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sequence of primer F was based

<400> 27  
Gln Xaa Xaa Xaa Arg Trp Trp  
1 5

<210> 28  
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<223> Description of Artificial Sequence: conserved  
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was based wherein Xaa at position 6 represents Phe or Leu

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sequence of primer G was based

<400> 28  
Asp Val Ile Lys Gly Xaa Asn Trp  
1 5

<210> 29  
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<213> Artificial Sequence

<220>  
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aattaaccct cactaaaggg

20

<210> 30  
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<212> DNA  
<213> Artificial Sequence

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oligonucleotide primer sequence

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gtaatacgac tcactatagg gc

22

<210> 31  
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 <212> DNA  
 <213> Abies grandis

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 <223> Clone AG3.48

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 Met  
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gct ctg gtt tct atc tca ccg ttg gct tcg aaa tct tgc ctg cgc aag 107  
 Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys Leu Arg Lys  
 5 10 15

tcg ttg atc agt tca att cat gaa cat aag cct ccc tat aga aca atc 155  
 Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr Arg Thr Ile  
 20 25 30

cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg cct tcc atg 203  
 Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr Pro Ser Met  
 35 40 45

agc atc agt ttg gcc acc gct gca cct gat gat ggt gta caa aga cgc 251  
 Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg Arg  
 50 55 60 65

ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc ata cag tct 299  
 Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln Ser  
 70 75 80

cta tca acg cat tat ggg gaa ccc tct tac cag gaa cgt gct gag aga 347  
 Leu Ser Thr His Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu Arg  
 85 90 95

tta att gtg gag gta aag aag ata ttc aat tca atg tac ctg gat gat 395  
 Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp Asp  
 100 105 110

gga aga tta atg agt tcc ttt aat gat ctc atg caa cgc ctt tgg ata 443  
 Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp Ile  
 115 120 125

gtc gat agc gtt gaa cgt ttg ggg ata gct aga cat ttc aag aac gag 491  
 Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn Glu  
 130 135 140 145

ata aca tca gct ctg gat tat gtt ttc cgt tac tgg gag gaa aac ggc 539  
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att gga tgt ggg aga gac agt att gtt act gat ctc aac tca act gcg 587  
 Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr Ala  
 165 170 175

ttg ggg ttt cga act ctt cga tta cac ggg tac act gta tct cca gag 635

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Leu	Gly	Phe	Arg	Thr	Leu	Arg	Leu	His	Gly	Tyr	Thr	Val	Ser	Pro	Glu		
		180					185					190					
ggt	tta	aaa	gct	ttt	caa	gat	caa	aat	gga	cag	ttt	gta	tgc	tcc	ccc	683	
Val	Leu	Lys	Ala	Phe	Gln	Asp	Gln	Asn	Gly	Gln	Phe	Val	Cys	Ser	Pro		
	195					200				205							
ggt	cag	aca	gag	ggt	gag	atc	aga	agc	ggt	ctt	aac	tta	tat	cgg	gct	731	
Gly	Gln	Thr	Glu	Gly	Glu	Ile	Arg	Ser	Val	Leu	Asn	Leu	Tyr	Arg	Ala		
	210				215				220					225			
tcc	ctc	att	gcc	ttc	cct	ggt	gag	aaa	ggt	atg	gaa	gaa	gct	gaa	atc	779	
Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu	Glu	Ala	Glu	Ile		
			230						235					240			
ttc	tcc	aca	aga	tat	ttg	aaa	gaa	gct	cta	caa	aag	att	cca	gtc	tcc	827	
Phe	Ser	Thr	Arg	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Lys	Ile	Pro	Val	Ser		
			245					250					255				
gct	ctt	tca	caa	gag	ata	aag	ttt	ggt	atg	gaa	tat	ggc	tgg	cac	aca	875	
Ala	Leu	Ser	Gln	Glu	Ile	Lys	Phe	Val	Met	Glu	Tyr	Gly	Trp	His	Thr		
		260					265					270					
aat	ttg	cca	aga	ttg	gaa	gca	aga	aat	tac	ata	gac	aca	ctt	gag	aaa	923	
Asn	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Asp	Thr	Leu	Glu	Lys		
	275					280					285						
gac	acc	agt	gca	tgg	ctc	aat	aaa	aat	gct	ggg	aag	aag	ctt	tta	gaa	971	
Asp	Thr	Ser	Ala	Trp	Leu	Asn	Lys	Asn	Ala	Gly	Lys	Lys	Leu	Leu	Glu		
	290				295				300						305		
ctt	gca	aaa	ttg	gag	ttc	aat	ata	ttt	aac	tcc	tta	caa	caa	aag	gaa	1019	
Leu	Ala	Lys	Leu	Glu	Phe	Asn	Ile	Phe	Asn	Ser	Leu	Gln	Gln	Lys	Glu		
			310					315						320			
tta	caa	tat	ctt	ttg	aga	tgg	tgg	aaa	gag	tcg	gat	ttg	cct	aaa	ttg	1067	
Leu	Gln	Tyr	Leu	Leu	Arg	Trp	Trp	Lys	Glu	Ser	Asp	Leu	Pro	Lys	Leu		
			325					330					335				
aca	ttt	gct	cgg	cat	cgt	cat	gtg	gaa	ttc	tac	act	ttg	gcc	tct	tgt	1115	
Thr	Phe	Ala	Arg	His	Arg	His	Val	Glu	Phe	Tyr	Thr	Leu	Ala	Ser	Cys		
		340					345					350					
att	gcc	att	gac	cca	aaa	cat	tct	gca	ttc	aga	cta	ggc	ttc	gcc	aaa	1163	
Ile	Ala	Ile	Asp	Pro	Lys	His	Ser	Ala	Phe	Arg	Leu	Gly	Phe	Ala	Lys		
	355					360					365						
atg	tgt	cat	ctt	gtc	aca	ggt	ttg	gac	gat	att	tac	gac	act	ttt	gga	1211	
Met	Cys	His	Leu	Val	Thr	Val	Leu	Asp	Asp	Ile	Tyr	Asp	Thr	Phe	Gly		
	370				375				380					385			
acg	att	gac	gag	ctt	gaa	ctc	ttc	aca	tct	gca	att	aag	aga	tgg	aat	1259	
Thr	Ile	Asp	Glu	Leu	Glu	Leu	Phe	Thr	Ser	Ala	Ile	Lys	Arg	Trp	Asn		
			390					395						400			
tca	tca	gag	ata	gaa	cac	ctt	cca	gaa	tat	atg	aaa	tgt	gtg	tac	atg	1307	
Ser	Ser	Glu	Ile	Glu	His	Leu	Pro	Glu	Tyr	Met	Lys	Cys	Val	Tyr	Met		
			405					410					415				
gtc	gtg	ttt	gaa	act	gta	aat	gaa	ctg	aca	cga	gag	gcg	gag	aag	act	1355	
Val	Val	Phe	Glu	Thr	Val	Asn	Glu	Leu	Thr	Arg	Glu	Ala	Glu	Lys	Thr		

[illegible]

<210> 32  
 <211> 627  
 <212> PRT  
 <213> Abies grandis

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 Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr Arg Thr  
 20 25 30  
 Ile Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr Pro Ser  
 35 40 45  
 Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg  
 50 55 60  
 Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln  
 65 70 75 80  
 Ser Leu Ser Thr His Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu  
 85 90 95  
 Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp  
 100 105 110  
 Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp  
 115 120 125  
 Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn  
 130 135 140  
 Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn  
 145 150 155 160  
 Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr  
 165 170 175  
 Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val Ser Pro  
 180 185 190  
 Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val Cys Ser  
 195 200 205  
 Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu Tyr Arg  
 210 215 220  
 Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu  
 225 230 235 240  
 Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro Val  
 245 250 255  
 Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly Trp His  
 260 265 270  
 Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr Leu Glu  
 275 280 285



Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys Leu Leu  
 290 295 300  
 Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln Gln Lys  
 305 310 315 320  
 Glu Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu Pro Lys  
 325 330 335  
 Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu Ala Ser  
 340 345 350  
 Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala  
 355 360 365  
 Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe  
 370 375 380  
 Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp  
 385 390 395 400  
 Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr  
 405 410 415  
 Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala Glu Lys  
 420 425 430  
 Thr Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp Glu Ala  
 435 440 445  
 Tyr Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr  
 450 455 460  
 Leu Pro Thr Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala  
 465 470 475 480  
 Tyr Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu  
 485 490 495  
 Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp  
 500 505 510  
 Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys  
 515 520 525  
 Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met  
 530 535 540  
 Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn  
 545 550 555 560  
 Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg  
 565 570 575  
 Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile  
 580 585 590  
 Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val  
 595 600 605  
 Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu Glu Ser

610

615

620

Met Leu Phe  
625

<210> 33

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR  
oligonucleotide primer 2.2 BamHI

<400> 33

caaagggatc cagaatggct ctgg

24

<210> 34

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR  
oligonucleotide primer 2.2 Not I

<400> 34

agtaagcggc cgctttttaa tcataccac

30

<210> 35

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR  
oligonucleotide primer 3.18 EcoRI

<400> 35

ctgcaggaat tcggcacgag c

21

<210> 36

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR  
oligonucleotide primer 3.18 SmaI

<400> 36

catagccccg ggcatagatt tgagctg

27

<210> 37

<211> 30

<212> DNA



<210> 42  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR  
 oligonucleotide primer 3-11

<400> 42  
 cgtaatggaa agctctggcg 20

<210> 43  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR  
 oligonucleotide primer 7-1

<400> 43  
 ccttacacgc ctttgatgg 20

<210> 44  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR  
 oligonucleotide sequence 7-3

<400> 44  
 tctgttgatc caggatggtc 20

<210> 45  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: conserved  
 amino acid motif common to all prenyl transferases wherein Xaa at  
 position  
 3 and 4 represents any amino acid

<400> 45  
 Asp Asp Xaa Xaa Asp  
 1 5

<210> 46  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

Sequence

<220>

<223> Description of Artificial Sequence: amino acid motif from which oligonucleotide primers can be synthesized that hybridize to the monoterpene synthases of the present invention, wherein Xaa at position 4 represents  
Leu or Ile or Val

<400> 46

His Ser Asn Xaa Trp Asp Asp Asp  
1 5

<210> 47

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotides can be constructed that hybridize to the monoterpene synthases of the present invention

<400> 47

Ala Leu Asp Tyr Val Tyr  
1 5

<210> 48

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotide sequences can be constructed that hybridize to the monoterpene synthases of the present invention

<400> 48

Glu Leu Ala Lys Leu Glu Phe  
1 5

<210> 49

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotide sequences can be constructed that hybridize to monoterpene synthase clones of the present invention

<400> 49

Arg Trp Trp Lys Glu Ser  
1 5

<210> 50  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: amino acid  
motif from which oligonucleotide sequences can be  
constructed that hybridize to monoterpene synthase  
clones of the present invention, wherein Xaa at position 1 represents  
Val  
or Ile or Leu

<400> 50  
Xaa Leu Asp Asp Met Tyr Asp  
1 5

<210> 51  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: amino acid  
motif from which oligonucleotide sequences can be  
constructed that hybridize to monoterpene synthase  
clones of the present invention wherein Xaa at position 1 represents  
Val  
or Ile or Leu

<400> 51  
Xaa Leu Asp Asp Leu Tyr Asp  
1 5

<210> 52  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: amino acid  
motif from which oligonucleotide sequences can be  
constructed that hybridize to the monoterpene  
synthase clones of the present invention, wherein Xaa at position 1  
represents Val or Ile or Leu

<400> 52  
Xaa Leu Asp Asp Ile Tyr Asp  
1 5

<210> 53  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: amino acid

motif from which oligonucleotide sequences can be constructed that hybridize to the monoterpene synthase clones of the present invention, wherein Xaa at position 6 represents Asn or His

<400> 53

Cys Tyr Met Lys Asp Xaa Pro  
1 5

<210> 54

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: exemplary oligonucleotide that corresponds to peptide sequence MetMetMet

<400> 54

atgatgatg

9

<210> 55

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: exemplary oligonucleotide sequence that corresponds to peptide sequence MetMetMet

<400> 55

tactactac

9

<210> 56

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: exemplary oligonucleotide that corresponds to peptide sequence MetMetMet, n is inosine

<400> 56

nacnacnac

9

<210> 57

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: oligonucleotide corresponding to amino acid sequence set forth in SEQ ID NO:46

<220>  
<221> misc\_feature  
<222> (1)..(24)  
<223> Oligonucleotide that corresponds to the conserved  
amino acid sequence set forth in SEQ ID NO:46

<400> 57  
gtgtcgttgg agaccctgct gctg

24

<210> 58  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide sequence corresponding to amino  
acid sequence set forth in SEQ ID NO:47

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<221> misc\_feature  
<222> (1)..(18)  
<223> Oligonucleotide corresponding to amino acid  
sequence set forth in SEQ ID NO:47

<400> 58  
cgggagctga tgcagatg

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<210> 59  
<211> 21  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:  
oligonucleotide that corresponds to amino acid  
sequence set forth in SEQ ID NO:48

<220>  
<221> misc\_feature  
<222> (1)..(21)  
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amino acid sequence set forth in SEQ ID NO:48

<400> 59  
ctcgagcggg togagctcaa g

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<210> 60  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide that corresponds to amino acid  
sequence set forth in SEQ ID NO:49



<220>  
 <221> misc\_feature  
 <222> (1)..(18)  
 <223> Oligonucleotide that corresponds to conserved  
 amino acid sequence set forth in SEQ ID NO:49

<400> 60  
 gccaccacct tcctctcg 18

<210> 61  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 oligonucleotide sequence corresponding to amino  
 acid sequence set forth in SEQ ID NO:50

<220>  
 <221> misc\_feature  
 <222> (1)..(21)  
 <223> Oligonucleotide sequence corresponding to amino  
 acid sequence set forth in SEQ ID NO:50

<400> 61  
 gaggagctgc tgtacatgct g 21

<210> 62  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 oligonucleotide corresponding to amino acid  
 sequence set forth in SEQ ID NO:51

<220>  
 <221> misc\_feature  
 <222> (1)..(21)  
 <223> Oligonucleotide corresponding to conserved amino  
 acid sequence set forth in SEQ ID NO:51

<400> 62  
 gaggagctgc tggagatgct g 21

<210> 63  
 <211> 293  
 <212> DNA  
 <213> Abies grandis

<400> 63  
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 cgcaatgctt atgagtctca ttttgattcg tttatgcacg aagcaaaatg gatctcaagt 120

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ggttatctcc caacgtttga ggagtacttg aagaatggga aagttagttc cggttctcgc 180  
 acagccactt tacaacccat actcaccttg gatgtaccac ttctaatta catactgcaa 240  
 gaaattgatt atccatctag gttcaatgac ttggcttcgt ccctccttcg cta 293

<210> 64  
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 <212> DNA  
 <213> Abies grandis

<220>  
 <221> CDS  
 <222> (36)..(1889)

<400> 64  
 ttttgacgtg ccttcttata tgatagcaag ctgaa atg gct ctt ctt tct att 53  
 Met Ala Leu Leu Ser Ile  
 1 5

act ccg ctg gtt tcc agg tcg tgc ctc agt tct tct cat gag att aag 101  
 Thr Pro Leu Val Ser Arg Ser Cys Leu Ser Ser Ser His Glu Ile Lys  
 10 15 20

gct ctc cgt aga aca atc cca act ctt gga atc tgc agg ccg ggg aaa 149  
 Ala Leu Arg Arg Thr Ile Pro Thr Leu Gly Ile Cys Arg Pro Gly Lys  
 25 30 35

tcc gtc gcg cat tcc ata aac atg tgt ttg aca agc gtc gca tct act 197  
 Ser Val Ala His Ser Ile Asn Met Cys Leu Thr Ser Val Ala Ser Thr  
 40 45 50

gat tct gta cag aga cgc gtg ggc aac tat cat tcc aac ctg tgg gac 245  
 Asp Ser Val Gln Arg Arg Val Gly Asn Tyr His Ser Asn Leu Trp Asp  
 55 60 65 70

gat gat ttc ata cag tct ctg atc tca acg cct tat gga gca cct gat 293  
 Asp Asp Phe Ile Gln Ser Leu Ile Ser Thr Pro Tyr Gly Ala Pro Asp  
 75 80 85

tac ccg gaa cgt gct gac aga ctt att ggg gaa gta aag gat ata atg 341  
 Tyr Arg Glu Arg Ala Asp Arg Leu Ile Gly Glu Val Lys Asp Ile Met  
 90 95 100

ttc aat ttc aag tcg ctg gaa gat gga ggc aat gat ctc ctt caa cga 389  
 Phe Asn Phe Lys Ser Leu Glu Asp Gly Gly Asn Asp Leu Leu Gln Arg  
 105 110 115

ctt ttg ctg gtc gat gac gtt gaa cgt ttg gga atc gac agg cat ttc 437  
 Leu Leu Leu Val Asp Asp Val Glu Arg Leu Gly Ile Asp Arg His Phe  
 120 125 130

aaa aaa gag ata aaa acg gca ctc gat tat gtt aac agt tat tgg aac 485  
 Lys Lys Glu Ile Lys Thr Ala Leu Asp Tyr Val Asn Ser Tyr Trp Asn  
 135 140 145 150

gaa aaa ggc att gga tgt ggg agg gag agt gtt gtg act gac ctc aac 533  
 Glu Lys Gly Ile Gly Cys Gly Arg Glu Ser Val Val Thr Asp Leu Asn  
 155 160 165

400 64  
 ttttgacgtg ccttcttata tgatagcaag ctgaa atg gct ctt ctt tct att 53  
 Met Ala Leu Leu Ser Ile  
 1 5

tca acc gcc ttg ggg ctt cga act ctc cga cta cac gga tac act gtg	581
Ser Thr Ala Leu Gly Leu Arg Thr Leu Arg Leu His Gly Tyr Thr Val	
170 175 180	
tct tca gat gtt ttg aac gtt ttt aaa gac aaa aat ggg caa ttt tcc	629
Ser Ser Asp Val Leu Asn Val Phe Lys Asp Lys Asn Gly Gln Phe Ser	
185 190 195	
tcc act gcc aat att cag ata gag gga gag att aga ggc gtt ctc aat	677
Ser Thr Ala Asn Ile Gln Ile Glu Gly Glu Ile Arg Gly Val Leu Asn	
200 205 210	
tta ttc agg gcc tcc ctc gtc gcc ttt ccc ggc gag aaa gtt atg gat	725
Leu Phe Arg Ala Ser Leu Val Ala Phe Pro Gly Glu Lys Val Met Asp	
215 220 225 230	
gaa gct gaa aca ttc tct aca aaa tat tta aga gaa gcc ctg caa aag	773
Glu Ala Glu Thr Phe Ser Thr Lys Tyr Leu Arg Glu Ala Leu Gln Lys	
235 240 245	
att ccg gca tcc agt ata ctt tca cta gag ata cgg gac gtt ctg gaa	821
Ile Pro Ala Ser Ser Ile Leu Ser Leu Glu Ile Arg Asp Val Leu Glu	
250 255 260	
tat ggt tgg cac acc aat ttg cca cgc ttg gaa gca agg aat tac atg	869
Tyr Gly Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Met	
265 270 275	
gac gtc ttt gga cag cac act aaa aat aag aac gcc gcc gag aaa ctt	917
Asp Val Phe Gly Gln His Thr Lys Asn Lys Asn Ala Ala Glu Lys Leu	
280 285 290	
tta gaa ctt gca aaa ttg gaa ttc aat ata ttt cac tcc tta caa gag	965
Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu Gln Glu	
295 300 305 310	
aga gag tta aaa cat gtt tcc cga tgg tgg aaa gac tcg ggt tct cct	1013
Arg Glu Leu Lys His Val Ser Arg Trp Trp Lys Asp Ser Gly Ser Pro	
315 320 325	
gag atg acc ttc tgt cga cat cgt cac gtg gaa tac tac gct ttg gct	1061
Glu Met Thr Phe Cys Arg His Arg His Val Glu Tyr Tyr Ala Leu Ala	
330 335 340	
tcc tgc att gcg ttc gag cct caa cat tct gga ttc aga ctc ggc ttt	1109
Ser Cys Ile Ala Phe Glu Pro Gln His Ser Gly Phe Arg Leu Gly Phe	
345 350 355	
acc aag atg tct cat ctt atc acg gtt ctt gac gac atg tac gac gtc	1157
Thr Lys Met Ser His Leu Ile Thr Val Leu Asp Asp Met Tyr Asp Val	
360 365 370	
ttc ggc aca gta gac gag ctg gaa ctc ttc aca gcg aca att aag aga	1205
Phe Gly Thr Val Asp Glu Leu Glu Leu Phe Thr Ala Thr Ile Lys Arg	
375 380 385 390	
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Trp Asp Pro Ser Ala Met Glu Cys Leu Pro Glu Tyr Met Lys Gly Val	
395 400 405	
tac atg atg gtt tat cac acc gta aat gaa atg gct cga gtg gca gag	1301

4 10 16 22 28 34 40 46 52 58 64 70 76 82 88 94 100 106 112 118 124 130 136 142 148 154 160 166 172 178 184 190 196 202 208 214 220 226 232 238 244 250 256 262 268 274 280 286 292 298 304 310 316 322 328 334 340 346 352 358 364 370 376 382 388 394 400 406 412 418 424 430 436 442 448 454 460 466 472 478 484 490 496 502 508 514 520 526 532 538 544 550 556 562 568 574 580 586 592 598 604 610 616 622 628 634 640 646 652 658 664 670 676 682 688 694 700 706 712 718 724 730 736 742 748 754 760 766 772 778 784 790 796 802 808 814 820 826 832 838 844 850 856 862 868 874 880 886 892 898 904 910 916 922 928 934 940 946 952 958 964 970 976 982 988 994

Tyr Met Met Val Tyr His Thr Val Asn Glu Met Ala Arg Val Ala Glu	
410 415 420	
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Lys Ala Gln Gly Arg Asp Thr Leu Asn Tyr Ala Arg Gln Ala Trp Glu	
425 430 435	
gcg tgt ttt gat tcg tat atg cag gaa gca aag tgg atc gcc act ggt	1397
Ala Cys Phe Asp Ser Tyr Met Gln Glu Ala Lys Trp Ile Ala Thr Gly	
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Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Glu Asn Gly Lys Val Ser Ser	
455 460 465 470	
gct cat cgc cca tgc gca ctg caa ccc att ctg acg ttg gac atc ccc	1493
Ala His Arg Pro Cys Ala Leu Gln Pro Ile Leu Thr Leu Asp Ile Pro	
475 480 485	
ttt cct gat cac atc ctc aag gaa gtt gac ttc cca tcg aag ctc aat	1541
Phe Pro Asp His Ile Leu Lys Glu Val Asp Phe Pro Ser Lys Leu Asn	
490 495 500	
gac ttg ata tgt atc atc ctt cga tta aga ggt gat aca cgg tgc tac	1589
Asp Leu Ile Cys Ile Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr	
505 510 515	
aag gca gac agg gcc cgt gga gaa gaa gct tcg tct ata tca tgt tat	1637
Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ser Ile Ser Cys Tyr	
520 525 530	
atg aaa gac aat cct gga tta acg gaa gaa gat gct ctg aat cat atc	1685
Met Lys Asp Asn Pro Gly Leu Thr Glu Glu Asp Ala Leu Asn His Ile	
535 540 545 550	
aac ttc atg atc agg gac gca atc aga gaa tta aat tgg gag ctt cta	1733
Asn Phe Met Ile Arg Asp Ala Ile Arg Glu Leu Asn Trp Glu Leu Leu	
555 560 565	
aag cca gac aac agt gtt ccc atc act tcc aag aaa cac gca ttt gac	1781
Lys Pro Asp Asn Ser Val Pro Ile Thr Ser Lys Lys His Ala Phe Asp	
570 575 580	
ata agc aga gtt tgg cat cac ggt tac aga tac cga gat ggc tac agc	1829
Ile Ser Arg Val Trp His His Gly Tyr Arg Tyr Arg Asp Gly Tyr Ser	
585 590 595	
ttt gcc aac gtt gaa aca aag agt ttg gtg atg aga acc gtc att gaa	1877
Phe Ala Asn Val Glu Thr Lys Ser Leu Val Met Arg Thr Val Ile Glu	
600 605 610	
cct gtg cct ttg taacaacact tcaaactctac aatattaact gaggatgccc	1929
Pro Val Pro Leu	
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tgaaaaaaaaaaaaaaaaaaaa	2013

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 <213> Abies grandis

<400> 65

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			20					25					30		
Ile	Cys	Arg	Pro	Gly	Lys	Ser	Val	Ala	His	Ser	Ile	Asn	Met	Cys	Leu
		35					40					45			
Thr	Ser	Val	Ala	Ser	Thr	Asp	Ser	Val	Gln	Arg	Arg	Val	Gly	Asn	Tyr
	50					55					60				
His	Ser	Asn	Leu	Trp	Asp	Asp	Asp	Phe	Ile	Gln	Ser	Leu	Ile	Ser	Thr
65					70					75					80
Pro	Tyr	Gly	Ala	Pro	Asp	Tyr	Arg	Glu	Arg	Ala	Asp	Arg	Leu	Ile	Gly
				85				90						95	
Glu	Val	Lys	Asp	Ile	Met	Phe	Asn	Phe	Lys	Ser	Leu	Glu	Asp	Gly	Gly
			100					105					110		
Asn	Asp	Leu	Leu	Gln	Arg	Leu	Leu	Leu	Val	Asp	Asp	Val	Glu	Arg	Leu
		115					120					125			
Gly	Ile	Asp	Arg	His	Phe	Lys	Lys	Glu	Ile	Lys	Thr	Ala	Leu	Asp	Tyr
	130					135					140				
Val	Asn	Ser	Tyr	Trp	Asn	Glu	Lys	Gly	Ile	Gly	Cys	Gly	Arg	Glu	Ser
145					150					155					160
Val	Val	Thr	Asp	Leu	Asn	Ser	Thr	Ala	Leu	Gly	Leu	Arg	Thr	Leu	Arg
				165					170					175	
Leu	His	Gly	Tyr	Thr	Val	Ser	Ser	Asp	Val	Leu	Asn	Val	Phe	Lys	Asp
			180					185					190		
Lys	Asn	Gly	Gln	Phe	Ser	Ser	Thr	Ala	Asn	Ile	Gln	Ile	Glu	Gly	Glu
		195					200					205			
Ile	Arg	Gly	Val	Leu	Asn	Leu	Phe	Arg	Ala	Ser	Leu	Val	Ala	Phe	Pro
	210					215					220				
Gly	Glu	Lys	Val	Met	Asp	Glu	Ala	Glu	Thr	Phe	Ser	Thr	Lys	Tyr	Leu
225					230					235					240
Arg	Glu	Ala	Leu	Gln	Lys	Ile	Pro	Ala	Ser	Ser	Ile	Leu	Ser	Leu	Glu
				245					250					255	
Ile	Arg	Asp	Val	Leu	Glu	Tyr	Gly	Trp	His	Thr	Asn	Leu	Pro	Arg	Leu
			260					265					270		
Glu	Ala	Arg	Asn	Tyr	Met	Asp	Val	Phe	Gly	Gln	His	Thr	Lys	Asn	Lys
		275					280					285			
Asn	Ala	Ala	Glu	Lys	Leu	Leu	Glu	Leu	Ala	Lys	Leu	Glu	Phe	Asn	Ile
		290				295					300				

Phe His Ser Leu Gln Glu Arg Glu Leu Lys His Val Ser Arg Trp Trp  
 305 310 315 320  
 Lys Asp Ser Gly Ser Pro Glu Met Thr Phe Cys Arg His Arg His Val  
 325 330 335  
 Glu Tyr Tyr Ala Leu Ala Ser Cys Ile Ala Phe Glu Pro Gln His Ser  
 340 345 350  
 Gly Phe Arg Leu Gly Phe Thr Lys Met Ser His Leu Ile Thr Val Leu  
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 Asp Asp Met Tyr Asp Val Phe Gly Thr Val Asp Glu Leu Glu Leu Phe  
 370 375 380  
 Thr Ala Thr Ile Lys Arg Trp Asp Pro Ser Ala Met Glu Cys Leu Pro  
 385 390 395 400  
 Glu Tyr Met Lys Gly Val Tyr Met Met Val Tyr His Thr Val Asn Glu  
 405 410 415  
 Met Ala Arg Val Ala Glu Lys Ala Gln Gly Arg Asp Thr Leu Asn Tyr  
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 Ala Arg Gln Ala Trp Glu Ala Cys Phe Asp Ser Tyr Met Gln Glu Ala  
 435 440 445  
 Lys Trp Ile Ala Thr Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Glu  
 450 455 460  
 Asn Gly Lys Val Ser Ser Ala His Arg Pro Cys Ala Leu Gln Pro Ile  
 465 470 475 480  
 Leu Thr Leu Asp Ile Pro Phe Pro Asp His Ile Leu Lys Glu Val Asp  
 485 490 495  
 Phe Pro Ser Lys Leu Asn Asp Leu Ile Cys Ile Ile Leu Arg Leu Arg  
 500 505 510  
 Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala  
 515 520 525  
 Ser Ser Ile Ser Cys Tyr Met Lys Asp Asn Pro Gly Leu Thr Glu Glu  
 530 535 540  
 Asp Ala Leu Asn His Ile Asn Phe Met Ile Arg Asp Ala Ile Arg Glu  
 545 550 555 560  
 Leu Asn Trp Glu Leu Leu Lys Pro Asp Asn Ser Val Pro Ile Thr Ser  
 565 570 575  
 Lys Lys His Ala Phe Asp Ile Ser Arg Val Trp His His Gly Tyr Arg  
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 Pro Lys Ser Cys Leu His Lys Ser Leu Ile Arg Ser Thr His His Glu  
 10 15 20

ctc aag cct ctg cgc aga acc atc cca act ctt gga atg tgt agg cga 150  
 Leu Lys Pro Leu Arg Arg Thr Ile Pro Thr Leu Gly Met Cys Arg Arg  
 25 30 35

ggg aaa tct ttc aca cct tct gtg agc atg agt ttg acc acc gct gta 198  
 Gly Lys Ser Phe Thr Pro Ser Val Ser Met Ser Leu Thr Thr Ala Val  
 40 45 50 55

tct gat gat ggt cta caa aga cgc ata ggt gac tat cat tcc aat ctc 246  
 Ser Asp Asp Gly Leu Gln Arg Arg Ile Gly Asp Tyr His Ser Asn Leu  
 60 65 70

tgg gac gac gat ttc ata cag tct cta tca acg cct tat ggg gag cct 294  
 Trp Asp Asp Asp Phe Ile Gln Ser Leu Ser Thr Pro Tyr Gly Glu Pro  
 75 80 85

tct tac cga gaa cgt gct gag aaa ctg att ggg gaa gtg aag gag atg 342  
 Ser Tyr Arg Glu Arg Ala Glu Lys Leu Ile Gly Glu Val Lys Glu Met  
 90 95 100

ttc aat tca atg cca tcg gaa gat gga gaa tca atg agt ccc ctc aat 390  
 Phe Asn Ser Met Pro Ser Glu Asp Gly Glu Ser Met Ser Pro Leu Asn  
 105 110 115

gat ctt att gaa cga ctt tgg atg gtc gat agc gtt gaa cgt ttg ggg 438  
 Asp Leu Ile Glu Arg Leu Trp Met Val Asp Ser Val Glu Arg Leu Gly  
 120 125 130 135

att gat aga cat ttc aaa aaa gag ata aaa tca gcc ctt gat tat gtt 486  
 Ile Asp Arg His Phe Lys Lys Glu Ile Lys Ser Ala Leu Asp Tyr Val  
 140 145 150

tac agt tat tgg aac gaa aaa ggt att gga tgc ggt aga gat agt gtt 534  
 Tyr Ser Tyr Trp Asn Glu Lys Gly Ile Gly Cys Gly Arg Asp Ser Val  
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ttt cct gat gtc aac tcg act gcc tcg ggg ttt cga act ctt cgc cta 582  
 Phe Pro Asp Val Asn Ser Thr Ala Ser Gly Phe Arg Thr Leu Arg Leu  
 170 175 180

cac gga tac agt gtc tct tca gag gtt ttg aaa gta ttt caa gac caa 630  
 His Gly Tyr Ser Val Ser Ser Glu Val Leu Lys Val Phe Gln Asp Gln

185	190	195	
aat ggg cag ttt gca ttc tct cct agt aca aaa gag aga gac atc aga			678
Asn Gly Gln Phe Ala Phe Ser Pro Ser Thr Lys Glu Arg Asp Ile Arg			
200	205	210	215
acc gtt ctg aat tta tat cgg gct tct ttc att gcc ttt cct ggg gag			726
Thr Val Leu Asn Leu Tyr Arg Ala Ser Phe Ile Ala Phe Pro Gly Glu			
	220	225	230
aaa gtt atg gaa gag gct gaa att ttc tct tca aga tat ttg aaa gaa			774
Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ser Arg Tyr Leu Lys Glu			
	235	240	245
gcc gtg caa aag att ccg gtc tcc agt ctt tca caa gaa ata gac tac			822
Ala Val Gln Lys Ile Pro Val Ser Ser Leu Ser Gln Glu Ile Asp Tyr			
	250	255	260
act ttg gaa tat ggt tgg cac aca aat atg cca aga ttg gaa aca agg			870
Thr Leu Glu Tyr Gly Trp His Thr Asn Met Pro Arg Leu Glu Thr Arg			
	265	270	275
aat tac tta gat gta ttt gga cat cct acc agt cca tgg ctc aag aag			918
Asn Tyr Leu Asp Val Phe Gly His Pro Thr Ser Pro Trp Leu Lys Lys			
280	285	290	295
aaa agg acg caa tat ctg gac agc gaa aag ctt tta gaa ctc gca aaa			966
Lys Arg Thr Gln Tyr Leu Asp Ser Glu Lys Leu Leu Glu Leu Ala Lys			
	300	305	310
ttg gag ttc aac atc ttt cac tcc ctt caa cag aag gag tta cag tat			1014
Leu Glu Phe Asn Ile Phe His Ser Leu Gln Gln Lys Glu Leu Gln Tyr			
	315	320	325
ctc tcc aga tgg tgg ata cat tcc ggt ttg cct gaa ctg acc ttt ggt			1062
Leu Ser Arg Trp Trp Ile His Ser Gly Leu Pro Glu Leu Thr Phe Gly			
	330	335	340
cgg cat cgt cac gtg gaa tac tac acc ctg agc tct tgc att gcg act			1110
Arg His Arg His Val Glu Tyr Tyr Thr Leu Ser Ser Cys Ile Ala Thr			
	345	350	355
gag ccc aaa cat tct gca ttc aga ttg ggc ttt gcc aaa acg tgt cat			1158
Glu Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala Lys Thr Cys His			
360	365	370	375
ctt atc acg gtt ctg gac gat atc tac gac act ttc gga acg atg gat			1206
Leu Ile Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly Thr Met Asp			
	380	385	390
gaa atc gaa ctc ttc aac gag gca gtt agg aga tgg aat ccg tcc gag			1254
Glu Ile Glu Leu Phe Asn Glu Ala Val Arg Arg Trp Asn Pro Ser Glu			
	395	400	405
aaa gaa cgc ctc cca gaa tat atg aaa gaa atc tac atg gca ctc tac			1302
Lys Glu Arg Leu Pro Glu Tyr Met Lys Glu Ile Tyr Met Ala Leu Tyr			
	410	415	420
gaa gcc tta act gac atg gcg cga gag gca gag aag aca caa ggc cga			1350
Glu Ala Leu Thr Asp Met Ala Arg Glu Ala Glu Lys Thr Gln Gly Arg			
425	430	435	

185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435



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 Asp Thr Leu Asn Tyr Ala Arg Lys Ala Trp Glu Val Tyr Leu Asp Ser  
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tat aca caa gaa gca aag tgg atc gcc agc ggt tat ctg cca act ttc 1446  
 Tyr Thr Gln Glu Ala Lys Trp Ile Ala Ser Gly Tyr Leu Pro Thr Phe  
 460 465 470

gag gag tac tta gag aac gcg aag gtt agc tct ggt cat cgt gca gcg 1494  
 Glu Glu Tyr Leu Glu Asn Ala Lys Val Ser Ser Gly His Arg Ala Ala  
 475 480 485

gca ttg aca ccc ctc ctg aca ttg gac gta ccg ctt cct gat gac gtc 1542  
 Ala Leu Thr Pro Leu Leu Thr Leu Asp Val Pro Leu Pro Asp Asp Val  
 490 495 500

ttg aag gga ata gat ttt cca tcg aga ttt aat gat ttg gca tct tcc 1590  
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 505 510 515

ttc ctt aga cta aga ggt gac aca cga tgc tac aag gca gac agg gac 1638  
 Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Asp  
 520 525 530 535

cga gga gaa gaa gcg tca agc ata tcg tgt tac atg aaa gac aat ccc 1686  
 Arg Gly Glu Glu Ala Ser Ser Ile Ser Cys Tyr Met Lys Asp Asn Pro  
 540 545 550

gga tta aca gag gaa gat gct ctc aat cat atc aat gcc atg atc aac 1734  
 Gly Leu Thr Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile Asn  
 555 560 565

gac ata atc aaa gaa tta aat tgg gaa ctt ctc aaa ccc gat agc aat 1782  
 Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Lys Pro Asp Ser Asn  
 570 575 580

att cca atg act gca cgg aaa cat gct tat gag ata acc aga gct ttc 1830  
 Ile Pro Met Thr Ala Arg Lys His Ala Tyr Glu Ile Thr Arg Ala Phe  
 585 590 595

cac caa ctt tac aaa tat aga gat ggc ttc agc gtt gcc act caa gaa 1878  
 His Gln Leu Tyr Lys Tyr Arg Asp Gly Phe Ser Val Ala Thr Gln Glu  
 600 605 610 615

acg aaa agt ttg gtg agg aga acg gtc ctt gaa cca gtg cct ctt 1923  
 Thr Lys Ser Leu Val Arg Arg Thr Val Leu Glu Pro Val Pro Leu  
 620 625 630

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catgtctctc tatgtaacta gttgtatgcg tggatatgatt ataaaattgg aggttactcg 2043

gtcctcacat ggtaatatgt gagttgtgaa attctcaaaa aaaaaaaaaa aaaaaaaaaa 2103

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aaaaaaaaaa aaaaaaaaaa aaa 2186

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Thr Ser Pro Trp Leu Lys Lys Lys Arg Thr Gln Tyr Leu Asp Ser Gl  
290 295 300

Lys Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu  
 305 310 315 320  
 Gln Gln Lys Glu Leu Gln Tyr Leu Ser Arg Trp Trp Ile His Ser Gly  
 325 330 335  
 Leu Pro Glu Leu Thr Phe Gly Arg His Arg His Val Glu Tyr Tyr Thr  
 340 345 350  
 Leu Ser Ser Cys Ile Ala Thr Glu Pro Lys His Ser Ala Phe Arg Leu  
 355 360 365  
 Gly Phe Ala Lys Thr Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr  
 370 375 380  
 Asp Thr Phe Gly Thr Met Asp Glu Ile Glu Leu Phe Asn Glu Ala Val  
 385 390 395 400  
 Arg Arg Trp Asn Pro Ser Glu Lys Glu Arg Leu Pro Glu Tyr Met Lys  
 405 410 415  
 Glu Ile Tyr Met Ala Leu Tyr Glu Ala Leu Thr Asp Met Ala Arg Glu  
 420 425 430  
 Ala Glu Lys Thr Gln Gly Arg Asp Thr Leu Asn Tyr Ala Arg Lys Ala  
 435 440 445  
 Trp Glu Val Tyr Leu Asp Ser Tyr Thr Gln Glu Ala Lys Trp Ile Ala  
 450 455 460  
 Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Glu Asn Ala Lys Val  
 465 470 475 480  
 Ser Ser Gly His Arg Ala Ala Ala Leu Thr Pro Leu Leu Thr Leu Asp  
 485 490 495  
 Val Pro Leu Pro Asp Asp Val Leu Lys Gly Ile Asp Phe Pro Ser Arg  
 500 505 510  
 Phe Asn Asp Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg  
 515 520 525  
 Cys Tyr Lys Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Ser Ile Ser  
 530 535 540  
 Cys Tyr Met Lys Asp Asn Pro Gly Leu Thr Glu Glu Asp Ala Leu Asn  
 545 550 555 560  
 His Ile Asn Ala Met Ile Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu  
 565 570 575  
 Leu Leu Lys Pro Asp Ser Asn Ile Pro Met Thr Ala Arg Lys His Ala  
 580 585 590  
 Tyr Glu Ile Thr Arg Ala Phe His Gln Leu Tyr Lys Tyr Arg Asp Gly  
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 Phe Ser Val Ala Thr Gln Glu Thr Lys Ser Leu Val Arg Arg Thr Val  
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Leu Glu Pro Val Pro Leu  
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Ser Leu Gln Val Pro Lys Ser Cys Gly Leu Lys Ser Leu Ile Ser Ser  
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agc aat gtg cag aag gct ctc tgt atc tct aca gca gtc cca act ctc 151  
Ser Asn Val Gln Lys Ala Leu Cys Ile Ser Thr Ala Val Pro Thr Leu  
25 30 35

aga atg cgt agg cga cag aaa gct ctg gtc atc aac atg aaa ttg acc 199  
Arg Met Arg Arg Arg Gln Lys Ala Leu Val Ile Asn Met Lys Leu Thr  
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act gta tcc cat cgt gat gat aat ggt ggt ggt gta ctg caa aga cgc 247  
Thr Val Ser His Arg Asp Asp Asn Gly Gly Gly Val Leu Gln Arg Arg  
60 65 70

ata gcc gat cat cat ccc aac ctg tgg gaa gat gat ttc ata caa tca 295  
Ile Ala Asp His His Pro Asn Leu Trp Glu Asp Asp Phe Ile Gln Ser  
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ttg tcc tca cct tat ggg gga tct tcg tac agt gaa cgt gct gtg aca 343  
Leu Ser Ser Pro Tyr Gly Gly Ser Ser Tyr Ser Glu Arg Ala Val Thr  
90 95 100

gtg gtt gag gaa gta aaa gag atg ttc aat tca ata cca aat aat aga 391  
Val Val Glu Glu Val Lys Glu Met Phe Asn Ser Ile Pro Asn Asn Arg  
105 110 115

gaa tta ttt ggt tcc caa aat gat ctc ctt aca cgc ctt tgg atg gtg 439  
Glu Leu Phe Gly Ser Gln Asn Asp Leu Leu Thr Arg Leu Trp Met Val  
120 125 130 135

gat agc att gaa cgt ctg ggg ata gat aga cat ttc caa aat gag ata 487  
Asp Ser Ile Glu Arg Leu Gly Ile Asp Arg His Phe Gln Asn Glu Ile  
140 145 150

aga gta gcc ctc gat tat gtt tac agt tat tgg aag gaa aag gaa ggc 535  
Arg Val Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Lys Glu Lys Glu Gly  
155 160 165

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Ile Gly Cys Gly Arg Asp Ser Thr Phe Pro Asp Leu Asn Ser Thr Ala  
170 175 180

117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

ctg gcg ctt cga act ctt cga ctg cac gga tac aat gtg tct tca gat	631
Leu Ala Leu Arg Thr Leu Arg Leu His Gly Tyr Asn Val Ser Ser Asp	
185 190 195	
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Val Leu Glu Tyr Phe Lys Asp Gln Lys Gly His Phe Ala Cys Pro Ala	
200 205 210 215	
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Ile Leu Thr Glu Gly Gln Ile Thr Arg Ser Val Leu Asn Leu Tyr Arg	
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gct tcc ctg gtc gcc ttt ccg ggg gag aaa gtt atg gaa gag gct gaa	775
Ala Ser Leu Val Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu	
235 240 245	
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Ile Phe Ser Ala Ser Tyr Leu Lys Glu Val Leu Gln Lys Ile Pro Val	
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Ser Ser Phe Ser Arg Glu Ile Glu Tyr Val Leu Glu Tyr Gly Trp His	
265 270 275	
aca aat ttg cca aga ttg gaa gca aga aat tat atc gac gtc tac ggg	919
Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Val Tyr Gly	
280 285 290 295	
cag gac agc tat gaa agt tca aac gag atg cca tat gtg aat acg cag	967
Gln Asp Ser Tyr Glu Ser Ser Asn Glu Met Pro Tyr Val Asn Thr Gln	
300 305 310	
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Lys Leu Leu Lys Leu Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu	
315 320 325	
caa cag aaa gag ttg caa tat atc tct aga tgg tgg aaa gat tcg tgt	1063
Gln Gln Lys Glu Leu Gln Tyr Ile Ser Arg Trp Trp Lys Asp Ser Cys	
330 335 340	
tca tct cat ctg act ttt act cga cac cgt cac gtg gaa tac tac aca	1111
Ser Ser His Leu Thr Phe Thr Arg His Arg His Val Glu Tyr Tyr Thr	
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Met Ala Ser Cys Ile Ser Met Glu Pro Lys His Ser Ala Phe Arg Leu	
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Gly Phe Val Lys Thr Cys His Leu Leu Thr Val Leu Asp Asp Met Tyr	
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gac act ttt gga aca ctg gac gaa ctc caa ctt ttt acg act gcc ttt	1255
Asp Thr Phe Gly Thr Leu Asp Glu Leu Gln Leu Phe Thr Thr Ala Phe	
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Lys Arg Trp Asp Leu Ser Glu Thr Lys Cys Leu Pro Glu Tyr Met Lys	
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425 430 435

gct gag aag act caa ggc aga gat acg ctc aac tat att cgc aat gct 1399  
Ala Glu Lys Thr Gln Gly Arg Asp Thr Leu Asn Tyr Ile Arg Asn Ala  
440 445 450 455

tat gag tct cat ttt gat tcg ttt atg cac gaa gca aaa tgg atc tca 1447  
Tyr Glu Ser His Phe Asp Ser Phe Met His Glu Ala Lys Trp Ile Ser  
460 465 470

agt ggt tat ctc cca acg ttt gag gag tac ttg aag aat ggg aaa gtt 1495  
Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Lys Asn Gly Lys Val  
475 480 485

agt tcc ggt tct cgc aca gcc act tta caa ccc ata ctc acc ttg gat 1543  
Ser Ser Gly Ser Arg Thr Ala Thr Leu Gln Pro Ile Leu Thr Leu Asp  
490 495 500

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Val Pro Leu Pro Asn Tyr Ile Leu Gln Glu Ile Asp Tyr Pro Ser Arg  
505 510 515

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Phe Asn Asp Leu Ala Ser Ser Leu Leu Arg Leu Arg Gly Asp Thr Arg  
520 525 530 535

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Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ala Ile Ser  
540 545 550

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Cys Tyr Met Lys Asp His Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn  
555 560 565

cat atc aac gtc atg atc agt gat gca atc aga gaa tta aat tgg gag 1783  
His Ile Asn Val Met Ile Ser Asp Ala Ile Arg Glu Leu Asn Trp Glu  
570 575 580

ctt ctc aga cca gat agc aaa agt ccc atc tct tcc aag aaa cat gct 1831  
Leu Leu Arg Pro Asp Ser Lys Ser Pro Ile Ser Ser Lys Lys His Ala  
585 590 595

ttt gac atc acc aga gct ttc cat cac ctc tac aag tac cga gat ggt 1879  
Phe Asp Ile Thr Arg Ala Phe His His Leu Tyr Lys Tyr Arg Asp Gly  
600 605 610 615

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Tyr Thr Val Ala Ser Ser Glu Thr Lys Asn Leu Val Met Lys Thr Val  
620 625 630

ctt gaa cct gtg gca ttg taaaaaata tcaaccgcat caaatgcac 1975  
Leu Glu Pro Val Ala Leu  
635

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 <212> PRT  
 <213> Abies grandis

<400> 69

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			20					25					30		
Ser	Thr	Ala	Val	Pro	Thr	Leu	Arg	Met	Arg	Arg	Arg	Gln	Lys	Ala	Leu
		35					40					45			
Val	Ile	Asn	Met	Lys	Leu	Thr	Thr	Val	Ser	His	Arg	Asp	Asp	Asn	Gly
	50					55					60				
Gly	Gly	Val	Leu	Gln	Arg	Arg	Ile	Ala	Asp	His	His	Pro	Asn	Leu	Trp
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Glu	Asp	Asp	Phe	Ile	Gln	Ser	Leu	Ser	Ser	Pro	Tyr	Gly	Gly	Ser	Ser
			85						90					95	
Tyr	Ser	Glu	Arg	Ala	Val	Thr	Val	Val	Glu	Glu	Val	Lys	Glu	Met	Phe
			100					105					110		
Asn	Ser	Ile	Pro	Asn	Asn	Arg	Glu	Leu	Phe	Gly	Ser	Gln	Asn	Asp	Leu
		115					120					125			
Leu	Thr	Arg	Leu	Trp	Met	Val	Asp	Ser	Ile	Glu	Arg	Leu	Gly	Ile	Asp
	130					135					140				
Arg	His	Phe	Gln	Asn	Glu	Ile	Arg	Val	Ala	Leu	Asp	Tyr	Val	Tyr	Ser
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Tyr	Trp	Lys	Glu	Lys	Glu	Gly	Ile	Gly	Cys	Gly	Arg	Asp	Ser	Thr	Phe
			165						170					175	
Pro	Asp	Leu	Asn	Ser	Thr	Ala	Leu	Ala	Leu	Arg	Thr	Leu	Arg	Leu	His
			180					185					190		
Gly	Tyr	Asn	Val	Ser	Ser	Asp	Val	Leu	Glu	Tyr	Phe	Lys	Asp	Gln	Lys
		195					200					205			
Gly	His	Phe	Ala	Cys	Pro	Ala	Ile	Leu	Thr	Glu	Gly	Gln	Ile	Thr	Arg
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Ser	Val	Leu	Asn	Leu	Tyr	Arg	Ala	Ser	Leu	Val	Ala	Phe	Pro	Gly	Glu

225	230	235	240
Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ala Ser Tyr Leu Lys Glu	245	250	255
Val Leu Gln Lys Ile Pro Val Ser Ser Phe Ser Arg Glu Ile Glu Tyr	260	265	270
Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg	275	280	285
Asn Tyr Ile Asp Val Tyr Gly Gln Asp Ser Tyr Glu Ser Ser Asn Glu	290	295	300
Met Pro Tyr Val Asn Thr Gln Lys Leu Leu Lys Leu Ala Lys Leu Glu	305	310	315
Phe Asn Ile Phe His Ser Leu Gln Gln Lys Glu Leu Gln Tyr Ile Ser	325	330	335
Arg Trp Trp Lys Asp Ser Cys Ser Ser His Leu Thr Phe Thr Arg His	340	345	350
Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser Met Glu Pro	355	360	365
Lys His Ser Ala Phe Arg Leu Gly Phe Val Lys Thr Cys His Leu Leu	370	375	380
Thr Val Leu Asp Asp Met Tyr Asp Thr Phe Gly Thr Leu Asp Glu Leu	385	390	395
Gln Leu Phe Thr Thr Ala Phe Lys Arg Trp Asp Leu Ser Glu Thr Lys	405	410	415
Cys Leu Pro Glu Tyr Met Lys Ala Val Tyr Met Asp Leu Tyr Gln Cys	420	425	430
Leu Asn Glu Leu Ala Gln Glu Ala Glu Lys Thr Gln Gly Arg Asp Thr	435	440	445
Leu Asn Tyr Ile Arg Asn Ala Tyr Glu Ser His Phe Asp Ser Phe Met	450	455	460
His Glu Ala Lys Trp Ile Ser Ser Gly Tyr Leu Pro Thr Phe Glu Glu	465	470	475
Tyr Leu Lys Asn Gly Lys Val Ser Ser Gly Ser Arg Thr Ala Thr Leu	485	490	495
Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asn Tyr Ile Leu Gln	500	505	510
Glu Ile Asp Tyr Pro Ser Arg Phe Asn Asp Leu Ala Ser Ser Leu Leu	515	520	525
Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Ala Arg Gly	530	535	540
Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His Pro Gly Ser	545	550	555
			560

1000 900 800 700 600 500 400 300 200 100 0



Thr Glu Glu Asp Ala Leu Asn His Ile Asn Val Met Ile Ser Asp Ala  
565 570 575

Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser Lys Ser Pro  
580 585 590

Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala Phe His His  
595 600 605

Leu Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ala Ser Ser Glu Thr Lys  
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<211> 696

<212> DNA

<213> Abies grandis

<400> 70

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cgagagacgc tcaacgatgc tcgacgagct tgggaggcct atcttgattc gtatatgaaa 180  
gaagctgagt ggatctccag tgggttatctg ccaacgtttg aggagtacat ggagaccagc 240  
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cttactcacc acatcctgca ggaaatagac ttccattga ggtttaatga cttaatatgt 360  
tccatccttc gacttaaaaa tgacactcgc tgctacaagg cggacagggc ccgtggagaa 420  
gaagcttcgt gtatatcgtg ttatatgaaa gagaatcctg gatcaacaga ggaagatgct 480  
atcaatcata tcaacgctat ggtcaataac ttaatcaaag aagtgaattg ggagcttctc 540  
cgacaggacg gcaccgctca tattgcttgc aagaaacacg cttttgacat cctcaaaggt 600  
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<211> 20

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1 5 10 15  
aaa tcg tgg atc gtt tct act tat gag cat aag gct atc agt aga aca 96  
Lys Ser Trp Ile Val Ser Thr Tyr Glu His Lys Ala Ile Ser Arg Thr  
20 25 30  
atc cca aat ctt gga ttg cgt ggg cga ggg aaa tct gtg aca cat tcc 144  
Ile Pro Asn Leu Gly Leu Arg Gly Arg Gly Lys Ser Val Thr His Ser  
35 40 45  
ctg aga atg agt ttg agc acc gca gtc tct gat gat cat ggt gta caa 192  
Leu Arg Met Ser Leu Ser Thr Ala Val Ser Asp Asp His Gly Val Gln  
50 55 60  
aga cgc ata gtc gag ttt cat tcc aat ctg tgg gac gac gat ttc ata 240

100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300

Arg	Arg	Ile	Val	Glu	Phe	His	Ser	Asn	Leu	Trp	Asp	Asp	Asp	Phe	Ile				
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Gln	Ser	Leu	Ser	Thr	Pro	Tyr	Gly	Ala	Pro	Ser	Tyr	Arg	Glu	Arg	Ala				
				85					90					95					
gat	aga	ctt	att	gtg	gaa	gta	aag	ggg	ata	ttc	act	tca	att	tca	gcg	336			
Asp	Arg	Leu	Ile	Val	Glu	Val	Lys	Gly	Ile	Phe	Thr	Ser	Ile	Ser	Ala				
			100					105					110						
gaa	gat	gga	gaa	cta	atc	act	ccc	ctc	aat	gat	ctc	att	caa	cgc	ctt	384			
Glu	Asp	Gly	Glu	Leu	Ile	Thr	Pro	Leu	Asn	Asp	Leu	Ile	Gln	Arg	Leu				
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tta	atg	gtc	gat	aac	gtt	gaa	cgt	tta	ggg	att	gat	aga	cat	ttc	aaa	432			
Leu	Met	Val	Asp	Asn	Val	Glu	Arg	Leu	Gly	Ile	Asp	Arg	His	Phe	Lys				
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aat	gag	ata	aaa	gca	gca	cta	gac	tat	gtt	tac	agt	tat	tgg	aac	gaa	480			
Asn	Glu	Ile	Lys	Ala	Ala	Leu	Asp	Tyr	Val	Tyr	Ser	Tyr	Trp	Asn	Glu				
		145			150					155					160				
aaa	ggc	att	ggc	agt	gga	agt	gat	agt	ggg	gtt	gct	gat	ctc	aac	tca	528			
Lys	Gly	Ile	Gly	Ser	Gly	Ser	Asp	Ser	Gly	Val	Ala	Asp	Leu	Asn	Ser				
				165				170						175					
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Thr	Ala	Leu	Gly	Phe	Arg	Ile	Leu	Arg	Leu	His	Gly	Tyr	Ser	Val	Ser				
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tca	gat	gtg	ttg	gaa	cac	ttc	aaa	gag	gag	aag	gag	aag	ggg	cag	ttt	624			
Ser	Asp	Val	Leu	Glu	His	Phe	Lys	Glu	Glu	Lys	Glu	Lys	Gly	Gln	Phe				
		195					200					205							
gta	tgt	tcg	gcc	atc	caa	aca	gag	gaa	gag	ata	aaa	agc	gtt	ctg	aat	672			
Val	Cys	Ser	Ala	Ile	Gln	Thr	Glu	Glu	Glu	Ile	Lys	Ser	Val	Leu	Asn				
		210				215					220								
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Leu	Phe	Arg	Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu				
		225			230					235				240					
gag	gct	gaa	atc	ttc	tct	aaa	ata	tat	tta	aaa	gaa	gcc	tta	caa	aat	768			
Glu	Ala	Glu	Ile	Phe	Ser	Lys	Ile	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Asn				
				245				250						255					
att	gct	gtc	tcc	agt	ctt	tca	cga	gag	ata	gag	tac	gtt	ctg	gag	gat	816			
Ile	Ala	Val	Ser	Ser	Leu	Ser	Arg	Glu	Ile	Glu	Tyr	Val	Leu	Glu	Asp				
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		275				280						285							
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Gln Gln Arg Glu Leu Lys Asp Leu Ser Arg Trp Trp Lys Asp Ser Gly	325	330	335	
ttc tct cac ctg aca ttt tct cgg cat cgt cat gtg gaa ttc tac gct				1056
Phe Ser His Leu Thr Phe Ser Arg His Arg His Val Glu Phe Tyr Ala	340	345	350	
ctg gca tct tgc att gaa act gat cgc aaa cat tcc gga ttc aga ctc				1104
Leu Ala Ser Cys Ile Glu Thr Asp Arg Lys His Ser Gly Phe Arg Leu	355	360	365	
ggc ttt gcc aaa atg tgt cat ctt atc acg gtt ttg gac gat ata tac				1152
Gly Phe Ala Lys Met Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr	370	375	380	
gac acc ttt gga aca atg gag gag ctg gaa ctc ttc act gca gca ttt				1200
Asp Thr Phe Gly Thr Met Glu Glu Leu Glu Leu Phe Thr Ala Ala Phe	385	390	395	400
aag aga tgg gat ccg tct gcc aca gat ttg ctt cca gag tat atg aaa				1248
Lys Arg Trp Asp Pro Ser Ala Thr Asp Leu Leu Pro Glu Tyr Met Lys	405	410	415	
ggg ttg tac atg gtg gtt tac gaa acc gta aat gaa att gct cga gag				1296
Gly Leu Tyr Met Val Val Tyr Glu Thr Val Asn Glu Ile Ala Arg Glu	420	425	430	
gca gac aag tct caa ggc cga gag acg ctc aac gat gct cga cga gct				1344
Ala Asp Lys Ser Gln Gly Arg Glu Thr Leu Asn Asp Ala Arg Arg Ala	435	440	445	
tgg gag gcc tat ctt gat tcg tat atg aaa gaa gct gag tgg atc tcc				1392
Trp Glu Ala Tyr Leu Asp Ser Tyr Met Lys Glu Ala Glu Trp Ile Ser	450	455	460	
agt ggt tat ctg cca acg ttt gag gag tac atg gag acc agc aaa gtt				1440
Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Met Glu Thr Ser Lys Val	465	470	475	480
agt ttt ggt tat cgc ata ttc gca ttg caa ccc atc ctc act atg gat				1488
Ser Phe Gly Tyr Arg Ile Phe Ala Leu Gln Pro Ile Leu Thr Met Asp	485	490	495	
gtt ccc ctt act cac cac atc ctg cag gaa ata gac ttt cca ttg agg				1536
Val Pro Leu Thr His His Ile Leu Gln Glu Ile Asp Phe Pro Leu Arg	500	505	510	
ttt aat gac tta ata tgt tcc atc ctt cga ctt aaa aat gac act cgc				1584
Phe Asn Asp Leu Ile Cys Ser Ile Leu Arg Leu Lys Asn Asp Thr Arg	515	520	525	
tgc tac aag gcg gac agg gcc cgt gga gaa gaa gct tcg tgt ata tcg				1632
Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Cys Ile Ser	530	535	540	
tgt tat atg aaa gag aat cct gga tca aca gag gaa gat gct atc aat				1680
Cys Tyr Met Lys Glu Asn Pro Gly Ser Thr Glu Glu Asp Ala Ile Asn	545	550	555	560

1008 1056 1104 1152 1200 1248 1296 1344 1392 1440 1488 1536 1584 1632 1680

cat atc aac gct atg gtc aat aac tta atc aaa gaa gtg aat tgg gag	1728
His Ile Asn Ala Met Val Asn Asn Leu Ile Lys Glu Val Asn Trp Glu	
565 570 575	
ctt ctc cga cag gac ggc acc gct cat att gct tgc aag aaa cac gct	1776
Leu Leu Arg Gln Asp Gly Thr Ala His Ile Ala Cys Lys Lys His Ala	
580 585 590	
ttt gac atc ctc aaa ggt tcc ctt cac ggc tac aaa tac cga gat ggg	1824
Phe Asp Ile Leu Lys Gly Ser Leu His Gly Tyr Lys Tyr Arg Asp Gly	
595 600 605	
ttc agc gtt gcc aac aag gaa acc aag aat tgg gtg agg aga aca gtc	1872
Phe Ser Val Ala Asn Lys Glu Thr Lys Asn Trp Val Arg Arg Thr Val	
610 615 620	
ctt gag tct gtg cct ttg	1890
Leu Glu Ser Val Pro Leu	
625 630	

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 20 25 30  
 Ile Pro Asn Leu Gly Leu Arg Gly Arg Gly Lys Ser Val Thr His Ser  
 35 40 45  
 Leu Arg Met Ser Leu Ser Thr Ala Val Ser Asp Asp His Gly Val Gln  
 50 55 60  
 Arg Arg Ile Val Glu Phe His Ser Asn Leu Trp Asp Asp Asp Phe Ile  
 65 70 75 80  
 Gln Ser Leu Ser Thr Pro Tyr Gly Ala Pro Ser Tyr Arg Glu Arg Ala  
 85 90 95  
 Asp Arg Leu Ile Val Glu Val Lys Gly Ile Phe Thr Ser Ile Ser Ala  
 100 105 110  
 Glu Asp Gly Glu Leu Ile Thr Pro Leu Asn Asp Leu Ile Gln Arg Leu  
 115 120 125  
 Leu Met Val Asp Asn Val Glu Arg Leu Gly Ile Asp Arg His Phe Lys  
 130 135 140  
 Asn Glu Ile Lys Ala Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Asn Glu  
 145 150 155 160  
 Lys Gly Ile Gly Ser Gly Ser Asp Ser Gly Val Ala Asp Leu Asn Ser  
 165 170 175

Thr Ala Leu Gly Phe Arg Ile Leu Arg Leu His Gly Tyr Ser Val Ser  
180 185 190

Ser Asp Val Leu Glu His Phe Lys Glu Glu Lys Glu Lys Gly Gln Phe  
195 200 205

Val Cys Ser Ala Ile Gln Thr Glu Glu Glu Ile Lys Ser Val Leu Asn  
210 215 220

Leu Phe Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu  
225 230 235 240

Glu Ala Glu Ile Phe Ser Lys Ile Tyr Leu Lys Glu Ala Leu Gln Asn  
245 250 255

Ile Ala Val Ser Ser Leu Ser Arg Glu Ile Glu Tyr Val Leu Glu Asp  
260 265 270

Gly Trp Gln Thr Asn Met Pro Arg Leu Glu Thr Arg Asn Tyr Ile Asp  
275 280 285

Val Leu Gly Glu Asn Asp Arg Asp Glu Thr Leu Tyr Met Asn Met Glu  
290 295 300

Lys Leu Leu Glu Ile Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu  
305 310 315 320

Gln Gln Arg Glu Leu Lys Asp Leu Ser Arg Trp Trp Lys Asp Ser Gly  
325 330 335

Phe Ser His Leu Thr Phe Ser Arg His Arg His Val Glu Phe Tyr Ala  
340 345 350

Leu Ala Ser Cys Ile Glu Thr Asp Arg Lys His Ser Gly Phe Arg Leu  
355 360 365

Gly Phe Ala Lys Met Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr  
370 375 380

Asp Thr Phe Gly Thr Met Glu Glu Leu Glu Leu Phe Thr Ala Ala Phe  
385 390 395 400

Lys Arg Trp Asp Pro Ser Ala Thr Asp Leu Leu Pro Glu Tyr Met Lys  
405 410 415

Gly Leu Tyr Met Val Val Tyr Glu Thr Val Asn Glu Ile Ala Arg Glu  
420 425 430

Ala Asp Lys Ser Gln Gly Arg Glu Thr Leu Asn Asp Ala Arg Arg Ala  
435 440 445

Trp Glu Ala Tyr Leu Asp Ser Tyr Met Lys Glu Ala Glu Trp Ile Ser  
450 455 460

Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Met Glu Thr Ser Lys Val  
465 470 475 480

Ser Phe Gly Tyr Arg Ile Phe Ala Leu Gln Pro Ile Leu Thr Met Asp  
485 490 495

Val Pro Leu Thr His His Ile Leu Gln Glu Ile Asp Phe Pro Leu Arg

500	505	510
Phe Asn Asp Leu Ile Cys Ser Ile Leu Arg Leu Lys Asn Asp Thr Arg 515	520	525
Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Cys Ile Ser 530	535	540
Cys Tyr Met Lys Glu Asn Pro Gly Ser Thr Glu Glu Asp Ala Ile Asn 545	550	555
His Ile Asn Ala Met Val Asn Asn Leu Ile Lys Glu Val Asn Trp Glu 565	570	575
Leu Leu Arg Gln Asp Gly Thr Ala His Ile Ala Cys Lys Lys His Ala 580	585	590
Phe Asp Ile Leu Lys Gly Ser Leu His Gly Tyr Lys Tyr Arg Asp Gly 595	600	605
Phe Ser Val Ala Asn Lys Glu Thr Lys Asn Trp Val Arg Arg Thr Val 610	615	620
Leu Glu Ser Val Pro Leu 625	630	

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<400> 79  
 caattaagag atgggacccg tccgcgatgg

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<210> 80  
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<210> 81  
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<400> 82  
ctgtggcaga cgggtcccat ctcttaaagt

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<210> 83  
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<400> 83  
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25

<210> 84  
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<400> 84  
ctgcgtattc acgtatggca tctcg

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<400> 85  
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<210> 86  
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<400> 86  
gcccacgcgt ctcatatgag aatcagtaga tgcg

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<210> 87  
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<400> 87

cacccatagg ggatcctcag ttaatatg

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<210> 88

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<400> 88

taagcgagca catatggctc tggtttcttc

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<210> 89

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<223> PCR primer 8-BamHI

<400> 89

gcataaacgc atagcgatc ctacaccaa

29

<210> 90

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<223> PCR primer 9-NdeI-M

<400> 90

cccggggatc ggacatatgg ctcttgtttc

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<210> 91

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<400> 91  
ggtcgactct agaggatcca ctagtgatat ggat

34

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<400> 92  
gaacatatgg ctctcctttc tatcgta

27

<210> 93  
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<400> 93  
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<210> 94  
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<400> 94  
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24

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<400> 96  
ctgatgatgg tcatatgaga cgcataagggtg

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<210> 97  
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<400> 97

gaccttatta ttatggatcc gggtatag

28

<210> 98  
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<400> 98  
ccgatgatgg tcatatgaga cgcattggcg

30

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<210> 100  
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<400> 101  
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24

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<210> 103  
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<400> 103  
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<210> 104  
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<210> 105  
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